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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2004, 09:59:31 ; Search time 21 Seconds
(without alignments)
2614.872 Million cell updates/sec

Title: US-09-978-194A-132

Perfect score: 3108
Sequence: 1 MLSSLVSLAGSVIWLIF.....PEPEAPGSCIANISQPTSC 571

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p11:*
2: p12:*
3: p13:*
4: p14:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	438.5	14.1	1524	2 T30337	polyprotein - Afri
2	437.5	14.1	343	1 A57014	proctasin (EC 3.4.
3	384.5	12.4	1004	2 T30338	oviductin (EC 3.4.
4	370.5	11.9	790	1 PLPG	plasma (EC 3.4.21
5	369.5	11.9	812	1 PLMS	plasma (EC 3.4.21
6	368.5	11.9	855	2 JC7731	membrane-bound arg
7	359.5	11.6	810	1 PLHU	plasma (EC 3.4.21
8	359	11.6	810	1 PLHU	plasma (EC 3.4.21
9	356.5	11.5	812	1 PLBO	plasma (EC 3.4.21
10	355.5	11.4	455	2 A61545	plasma (EC 3.4.21
11	353	11.4	417	1 S00845	hepsin (EC 3.4.21
12	351.5	11.3	810	2 B30848	plasma (EC 3.4.21
13	342	11.0	4548	1 S00657	apoptoferrin(a) (EC
14	339	10.9	1420	2 A32869	apolipoprotein(a)
15	338	10.9	460	2 B61545	plasma (EC 3.4.21
16	337.5	10.9	638	1 KQHP	plasma kallikrein
17	336	10.8	270	2 S56160	mast cell tryptase
18	335	10.8	275	2 A32410	tryptase (EC 3.4.2
19	333	10.7	276	2 A38654	mast cell proteina
20	330.5	10.6	273	2 A47246	tryptase (EC 3.4.2
21	330	10.6	271	2 A25528	pancreatic elastas
22	329	10.6	275	2 A35863	tryptase (EC 3.4.2
23	329	10.6	275	2 B35863	tryptase (EC 3.4.2
24	328.5	10.6	274	2 JC4171	tryptase (EC 3.4.2
25	328	10.6	275	2 C35863	tryptase (EC 3.4.2
26	327.5	10.5	366	2 JE0105	testicular serine
27	326.5	10.5	625	1 KFHU1	coagulation factor
28	326.5	10.5	638	1 KQMSPL	plasma kallikrein
29	325.5	10.5	263	1 KYRTB	chymotrypsin (EC 3

30	325.5	10.5	638	1 KQRTPL	plasma kallikrein
31	325	10.5	416	1 S33777	hepsin (EC 3.4.21
32	322.5	10.4	421	1 S11674	acrosin (EC 3.4.21
33	322	10.4	269	2 B26823	pancreatic elastas
34	322	10.4	269	2 A26823	pancreatic elastas
35	320.5	10.3	431	2 S47538	acrosin (EC 3.4.21
36	320	10.3	269	2 C26823	pancreatic elastas
37	320	10.3	271	1 ELRT2	pancreatic elastas
38	318.5	10.2	274	2 A45754	tryptase (EC 3.4.2
39	317.5	10.2	263	2 A21195	chymotrypsin (EC 3
40	317.5	10.2	761	2 JC5759	brain-specific ser
41	315.5	10.2	263	2 A21299	chymotrypsin (EC 3
42	315	10.1	1113	2 JE0315	low-density lipopr
43	313.5	10.1	245	1 KYBOA	chymotrypsin (EC 3
44	313	10.1	421	2 S29599	acrosin (EC 3.4.21
45	310.5	10.0	245	1 KYBOB	chymotrypsin (EC 3

ALIGNMENTS

RESULT 1					
T30337					
polyprotein - African clawed frog					
C:Species: Xenopus laevis (African clawed frog)					
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Feb-2003					
C:Accession: T30337					
R:Yang, J.C.; Lindsey, L.B.; Hedrick, J.L.					
submitted to the EMBL Data Library, March 1998					
A:Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from Xer					
A:Reference number: 220829					
A:Accession: T30337					
A:Status: preliminary; translated from GB/EMBL/DBJ					
A:Molecule type: mRNA					
A:Residues: 1-1524 <YAN>					
A:Cross-References: EMBL:U81290; NID:G2981640; PID:G2981641; PIDN:AAIC24717.1					
C:Superfamily: trypsin related polyprotein; trypsin homology					
Query Match					
Best Local Similarity 14.1% Score 438.5; DB 2; Length 1524;					
Matches 147; Conservative 97; Mismatches 211; Indels 327; Gaps 20;					
QY	59	GNTVGEWMPQASVRRQGAHICSGSLVADTWLTAHCFEKAATELMSWSVLGSLQRE	118		
DB	61	GDAVGGQPTVSLKLNERRHICGSIYRKDMVVAHCVVTEIKVSHMTVIGEYDQ	120		
QY	119	GLSPRAEYGVAAID-LPRAYNHYSQSDLAQLQALP-THTPICLPQPAHPPFG	173		
DB	121	VMDSQEQSIPVSHTEPHENYRGDGNMGYDIALVPLSKPIFGSOVQPCLPQVEKIEAG	180		
QY	174	ASCAATGMD--QDPSDARGTIRNLRLISRPTNCINQNHLSRPARFGMCGSPQ	231		
DB	181	TLCVSSGWLRENDLSVLOEVKLPVNDGTCGAVLEPIGHVPLDT--MLCAQFP	236		
QY	232	PGVQPCGSDGSPVLCLEPDGHVWQAGIISFPASSC--AQEDAPVLTN--	278		
DB	237	EGGMDACGSDGSPVVCRRGQWFLAGCVSWGCGSMWAKQIIRQSSSPALFASVS	296		
QY	279	-----TAHSS-----WQA-----	288		
DB	297	SULDPLRPPLKLTGGSSKGRITITGKNGTVRYPLSGNYSINVCWMLAVQAKITIEIRFL	356		
QY	289	-----	288		
DB	357	QUDIEDHATCTPDYLSFTVNEKMIKRVCGSTIPSPPLIVRSKKTVTFFSDGTFTGRGEI	416		
QY	289	-----RVQGAFLAQSPT-----	302		
DB	417	QFLAIPTRKAAGCSAKILKKKGMIYSFNPYDPYPRLKTCGMIIEAPNHHVKKLFEDFN	476		
QY	303	-----PENSDESCV-----	312		
DB	477	VEYHGICTYDAVEVYDGAEEKOLIAILCGYTLPLPISSPENTMILIRFKTDMENSGPGKV	536		

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QY 313 -----ACGSL-----RTGPGAGAPSPMP 331
DB 537 KESFVKEKQFSLPVDPTPTISMLHRAIALDYCGNAPMTPKWMLPRIVGGEASNSWP 596
QY 332 WEARLHQGLACGALVSEAVLTAAGFCIGQAEEMSVGLG-----TRPEMGL 383
DB 597 WQVQIFFLATPFCEGAIISFQWILTAHC-IRAAEFSYWTVAAGDNRMLNESTEOIRNI 655
QY 384 KOLILHGAAYTHPEBGYDMALLLAAQPVTLGASLRPLCLPYPDHHLDPGE---RGM--VL 437
DB 656 KTRIDHNVNSETRYDIDIALLYLEBPLDNDNFVRPVCLEPBEPEVLTNPASVCVVTGNGTA 715
QY 438 GRARPCAGISLQTVVTTLGPRACSRLLHAAPCGDSPLIPGMVCTSAV--GEL----- 489
DB 716 EDGQPALGLQQLQL-----PILDSIIICNTSYSGELTDHMLC 752
QY 490 ---PS-----CEGLSGAPLVHEVRGTWF-LAGLHSPGACCGPARPAFTLPAVEDMV 539
DB 753 AGPFSKEKXACGDSGGLVCONEKEQFSTYGLVSMGCGKRVSKPGVYTKVRLPFTWI 812
QY 540 SS 541
DB 813 QN 814

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RESULT 2
A57014
proctasin (EC 3.4.21.-) precursor - human
C/Species: Homo sapiens (man)
C/Date: 24-May-1996 #sequence_rev1sion 24-May-1996 #text_change 21-Apr-2003
C/Accession: A57014; A54866
R/Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 270, 13483-13489, 1995
A/Title: Molecular cloning, tissue-specific expression, and cellular localization of h
A/Reference number: A57014; MUID:95286644; PMID:7768952
A/Accession: A57014
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-343 <RES>
A/Cross-references: GB:I41351; NID:9862304; PIDN:AAC41759.1; PID:9862305
A/Experimental source: prostate
A/Note parts of this sequence were determined by protein sequencing
R/Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 269, 18843-18848, 1994
A/Title: Proctasin is a novel human serine proteinase from seminal fluid. Purification,
A/Reference number: A54866; MUID:94308140; PMID:8034638
A/Accession: A54866
A/Molecule type: protein
A/Residues: 45-64 <YUA>
C/Genetics:
A/Gene: GDB:PRSS8
A/Cross-references: GDB:676446; OMIM:600823
A/Map position: 16p11.2-16p11.2
C/Superfamily: trypsin; trypsin homology
C/Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
F.1-3/Domain: signal sequence #status predicted <SIG>
F.13-44/Domain: Product: proctasin #status predicted <MAT>
F.13-44/Domain: proctasin light chain #status predicted <CH>
F.45-343/Domain: proctasin heavy chain #status predicted <CH>
F.45-281/Domain: trypsin homology <TRY>
F.323-341/Domain: transmembrane #status predicted <TM>
F.137-154,70-86,168-244,201-223,234-262/Dissulfide bonds: #status predicted
F.85/34,238/Active site: His, Asp, Ser #status predicted
F.159/Binding site: carbonylate (Aen) (covalent) #status experimental

```

```

Query Match 14.1%; Score 437.5; DB 1; Length 343;
Best Local Similarity 35.3%; Pred. No. 2.1e-23;
Matches 110; Conservative 48; Mismatches 109; Indels 45; Gaps 14;

```

```

QY 51 PGKARHNTVPGEMQASVRQGAHICSGSLVADTWVLTAAHFEKKAATELNSWGV 110
DB 41 PQRITGSSAAVAGQWPMQVSTYEGVHVCGLVSEQWVLSAHCPSHHKE--AYEV 98

```

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QY 111 VIGSLQREGSLSPGAEVGAALQ--LPRAYNHSGS--DLALLQLAHPTHT---PLC 162
DB 99 KLGAHQQLSYS--BDAKYSTLKDIIPHP-SYLQESOGDIALLOLSRPTFSRYRPLC 154
QY 163 LPQAPHRPFGASCAWMDQDTS-----APCTLANLRLISRTNCINYLQHORHS 218
DB 155 LPAANASFPNGJHCVTGTHGVAHAPSVSLITRPLOOLEVPLISRTNCINVIDAKPEEP 214
QY 219 NPARPGLCGGPOPOVPGCGDSGGLVCLPDPGWVQAGIISPASSCAQEDAEVLLTN 278
DB 215 HPGQDMWCAGVBECKACGDSGGLPLC--PVELMLWLTGIVSGDAGCANRPGVTL 273
QY 279 TAHSQSWLQARY--QGAFLAQSPETPEMDESDSCVAGS-----LR----- 318
DB 274 ASSYASWIOSKVTETLQPRVV-----PQTOE-SQPDNL-CGSHLAFSAPAQGLRLPILFL 327
QY 319 TAGPQAGAPSPW 330
DB 328 PLGLALGLLSPW 339

```

```

RESULT 3
T30338
oviductin (EC 3.4.21.-) - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 22-Oct-1999 #sequence_rev1sion 22-Oct-1999 #text_change 03-Feb-2003
C/Accession: T30338; A40242
R/Lindsay, L.L.; Wieduwilt, M.J.; Hedrick, J.L.
Biol. Reprod. 60, 989-995, 1999
A/Title: Oviductin, the Xenopus laevis oviductal protease that processes egg envelope gl
A/Reference number: 220830; MUID:99184825; PMID:10084976
A/Accession: T30338
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1004 <LIN>
A/Cross-references: EMBL:081291; NID:91754713; PID:91754714; PIDN:AAB53972.1
R/Hardy, D.M.; Hedrick, J.L.
Biochemistry 31, 4466-4472, 1992
A/Title: Oviductin, purification and properties of the oviductal protease that processes
A/Reference number: A40242; MUID:92256375; PMID:1581303
A/Accession: A40242
A/Molecule type: protein
A/Residues: 46-73 <HAR>
C/Comment: This protease is found in oviductal secretory granules and is secreted to pro
C/Superfamily: oviductin; trypsin homology
C/Keywords: extracellular protein; hydrolase; serine proteinase

```

```

Query Match 12.4%; Score 384.5; DB 2; Length 1004;
Best Local Similarity 19.3%; Pred. No. 3.7e-19;
Matches 155; Conservative 92; Mismatches 232; Indels 325; Gaps 25;

```

```

QY 64 GEMPMQASVRQGAHICSGSLVADTWVLTAAHC-PEKKAATELNSWVSLQREGSLP 122
DB 55 GHPMTVALIKRNGKFCGGLTVSHCHVLTAAHCLLDNRVKKLYMR---VYIGEDY-QILKE 110
QY 123 GAEEV--GVAAQLQPRAYNHVSQGSDDLALQLAHPTHT---TPCLPQAPHRPFGASC 176
DB 111 ETEQAFRIETFKHNPQSQPMYDVAVLLDGSVTFDENIOPRCPLNPDVFEPPGLC 170
QY 177 WATGMDQDTSDA--PGLRLNRLRLISRPTNCINYLQHORHLSNPARPGLCGGPOPGV 234
DB 171 VTLGNGHITENGILPVLVQEVLPFVDSGSLHVMASLKGTVSS---YVCAQAFPGGG 226
QY 225 QCPGCGDSGGLVCLPDPGWVQAGIISPASSCA-----QEDAPVLLTNTAAH 282
DB 227 KDACCGDSGGLPCORRGSVTLHGLTSMGCGRSMKNVFLPHNRKSGSGLFTDIOKL 286
QY 283 SSWLARVQGA-- 294
DB 287 LGWSSQNTAVPNKNQSCSNQDGLSGKSGELIFLNPMSTVTRTMSGAPGFSLSLTKC 346

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Oy 295 -----FLA----- 297
Db 347 TSCNLFTHLIDESPACNLDYLAITYDSHRLIGKPCGDIIPRSLILSFSSIKLNFSDFH 406
Oy 298 -----OSPEPTE----- 304
Db 407 ENRTGFVLIVYSAVEPNNTYPDSCGCSFAVLFEFEGELQSNNTYENILSNRCHWIIHGPGS 466
Oy 305 -----MSDEDC-----VACG----- 315
Db 467 YIKLQFEDFALEPDDCDSDYLAAYQDLAEDKIETFCGSLPAPVYSTAWMIKFSTD 526
Oy 316 -----SLRTAGQACAPS----- 328
Db 527 ERDNKGRATFTFVPSNLSVEDSRQGMPTNKKETTAQDSICGVSPPIFYNSIAK 586
Oy 329 -----PMPEARLHMGGALACGALVSEAVLTAHCFTIGROAPEWSVGLG---TR 377
Db 587 VEEAVPHSMFPHNTSLQYAGEHVCDGAIITAEKWIITTTASCVLNRKNDVWLVDPGIHLIR 646
Oy 378 P-EEWGL-KQULIHGAYTHREGGYDMALLLLAQPVTLLGASLRPLCLPYRPHHLPDGE-- 432
Db 647 PGHNQKGLVKQIIPHSFSQTNDFDIALVELDESIGFNSDIPFLCLPFGKTSSELAPSLC 706
Oy 433 --RGVULGRAPGAGISLQTVPTLLGPACSRLLHA--PGDGSPLLPWVCTSAVG-- 487
Db 707 VVSGWML-RGKEAEKSTYLQOREVPIITDDACSAHYIKNPGG---ITDRMLC-AGIGTG 760
Oy 488 -ELDSGELSGAPLV--HEVGTWFLAGLSFGDCCGPARPAVFTALPAYEDWSSLDW 544
Db 761 QDNDSGCSQSSPLVCLLEKKGIYTFGSIASGVNCKENSKPGYITKVSPTDWTROI-- 818
Oy 545 QVYFAEPEPEAPEPCSLANISQP 568
Db 813 -----MSDTQGHNSNLGDP 832

```

RESULT 4

PLPG

plasmin (EC 3.4.21.7) precursor - pig (fragment)

N:Alternate names: plasminogen

C:Contains: miniplasminogen

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 07-Sep-1990 #sequence revision 01-Nov-1996 #text_change 18-Jul-1997

C:Accession: S03733; S03737; A25834

R:Schaller, J.; Marti, T.; Roesseler, S.J.; Kaempfer, U.; Rickli, E.E.

Fibrinolysis 1, 91-102, 1987

A:Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca

A:Reference number: S03733

A:Accession: S03733

A:Molecule type: protein

A:Residues: 1-560 <SCH>

R:Brunnholst, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Mameberg, M.

Eur. J. Biochem. 114, 465-470, 1981

A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,

A:Reference number: S03735; MUID:81212097; PMID:7238497

A:Accession: S03737

A:Molecule type: protein

A:Residues: 1-57 <SRU>

R:Marti, T.; Schaller, J.; Rickli, E.E.

Eur. J. Biochem. 149, 279-285, 1985

A:Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.

A:Reference number: A25834; MUID:85503907; PMID:3846533

A:Accession: A25834

A:Molecule type: protein

A:Residues: 450-790 <MAR>

C:Function:

A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va

A:Pathway: fibrinolysis

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote

F:1-790/Product: plasminogen #status predicted <PRO>

F:1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPG>
 F:1-77/Domain: activation peptide #status predicted <APT>
 F:78-560/Product: plasmin chain A #status predicted <ACH>
 F:166-162/Domain: kringle homology <KR1>
 F:166-243/Domain: kringle homology <KR2>
 F:166-333/Domain: kringle homology <KR3>
 F:358-435/Domain: kringle homology <KR4>
 F:450-790/Product: miniplasminogen #status experimental <MIN>
 F:461-540/Domain: kringle homology <KR5>
 F:561-790/Product: plasmin chain B #status experimental <BCH>
 F:561-783/Domain: trypsin homology <TRY>
 F:330-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305-
 bonds: #status predicted
 F:602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 11.9%; Score 370.5; DB 1; Length 790;
 Best Local Similarity 32.3%; Pred. No. 2,76-18;
 Matches 90; Conservative 49; Mismatches 101; Indels 39; Gaps 12;

```

Oy 23 LYDFCIV--CITYAINVSLMWLSF---RKVDEPGKAKRHGN--TVGEMWQASVR- 73
Db 531 LFQYCDVPQCVTS-----SFDGKPKVEBKCCPARVVGCVSIPIHSPWQISLRY 580
Oy 74 RQAHICSGSLVADTWLTLTAHCERKAATELNSMSVVLGSLQREGISPAHEVQVALQ 133
Db 581 RYRGHFCGGLTISPDEWVLTAKHCLKESSP--SSYKVIILGHEEYHLGEGVQETIDVSKL- 637
Oy 134 LPRAYNHSQSDALQLQNLHPTHT---PLCLPQPAHFPPFGASCATGMDODTSD-A 188
Db 638 ----FKEPSE-ADLALKLSSPAVITDKVIPACLPTRNYVAVDITACTITGMSTKGTG 692
Oy 189 PGLRLNLRLRLISRPNCIYNOLHQRHLSNPARPGLCGGPOPOVGOCGSGGPGVLC 248
Db 693 AGLLKEARLPVTEKVCN-----RYEYLGKQVGFNELCAGHLAGIDSCGDSGGLVVC 746
Oy 249 LEPDGHVQAGITSPASSCAQEDAPVLLTNTAAHSSMLQ 287
Db 747 FEKDKYILQ-GVTSWGLGCLPMKPGVYVRVSRPTWIE 784

```

RESULT 5

PLMS

plasmin (EC 3.4.21.7) precursor - mouse

N:Contains: angiotatin; plasminogen

C:Species: Mus musculus (house mouse)

C>Date: 20-Sep-1991 #sequence revision 01-Nov-1996 #text_change 18-Jun-1999

C:Accession: A38514; S48202; S48203

R:Deegen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.

Genomics 8, 49-61, 1990

A:Title: Characterization of the cDNA coding for mouse plasminogen and localization of cl

A:Reference number: A38514; MUID:91184812; PMID:2081600

A:Accession: A38514

A:Molecule type: mRNA

A:Residues: 1-812 <DEG>

A:Cross-references: GB:J04766; NID:G200402; PIDN:AAA50168.1; PID:G200403

R:Rilinen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.

Eur. J. Biochem. 224, 863-871, 1994

A:Title: Characterization of the murine plasma fibrinolytic system.

A:Reference number: S48202; MUID:95010076; PMID:7523120

A:Accession: S48202

A:Molecule type: protein

A:Residues: 20-25 <LIT>

A:Accession: S48203

A:Molecule type: protein

A:Residues: 22-27 <LIT>

C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many oth

C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

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C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin

A>Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A:Reference number: 145961; MUID:8502311; PMID:6148961
A:Accession: 162738
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 292-471, 'D', 473-810 <MAL2>
A:Cross-references: GB:K02992; NID:gl190112; PIDN:AAA60124.1; PID:gl387031
A:Accession: 184609
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 367-419 <MAL3>
A:Cross-references: GB:K02991; NID:gl190110; PIDN:AAA60123.1; PID:gl190111
R:Brundholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A>Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,
A:Reference number: S03735; MUID:81212097; PMID:7238497
A:Accession: S03735
A:Molecule type: protein
A:Residues: 20-71, 'E', 73-76 <BRU>
R:Sortrup-Jensen, L.; Petersen, T.E.; Magnusson, S.
submitted to the Atlas, July 1977
A:Reference number: A00929
A:Accession: A00929
A:Molecule type: protein
A:Residues: 20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>
R:Wiman, B.
Eur. J. Biochem. 76, 129-137, 1977
A>Title: Primary structure of the B-chain of human plasmin.
A:Reference number: A04627; MUID:77225245; PMID:142009
A:Accession: A04627
A:Molecule type: protein
A:Residues: 581-810 <W11>
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A>Title: Structural relationship between "glutamic acid" and "lysine" forms of human pla
A:Reference number: A04625; MUID:75093329; PMID:122932
A:Accession: A04625
A:Molecule type: protein
A:Residues: 20-50, 'Q', 51-71, 'E', 73-85, 87-100 <W12>
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A>Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha
A:Reference number: A04626; MUID:76043692; PMID:126863
A:Accession: A04626
A:Molecule type: protein
A:Residues: 483-507, 'E', 509-604 <W13>
R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
J. Biol. Chem. 248, 1631-1633, 1973
A>Title: The primary structure of human plasminogen. II. The histidine loop of human pla
A:Reference number: A92125; MUID:73149248; PMID:4694729
A:Contents: annotation; active site
R:Groskopf, W.R.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A>Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
A:Reference number: A92048; MUID:69234739; PMID:4240117
A:Contents: annotation; active site
R:Trexler, M.; Vail, Z.; Patchy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A>Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
A:Reference number: A92382; MUID:82213905; PMID:6919539
A:Contents: annotation; omega-aminocarboxylic acid binding sites
R:Vail, Z.; Patchy, L.
J. Biol. Chem. 259, 13690-13694, 1984
A>Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
A:Reference number: A92458; MUID:85054794; PMID:6094526
A:Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
R:Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.;
J. Biol. Chem. 271, 29461-29467, 1996
A>Title: Kringle domains of human angiotensin. Characterization of the anti-proliferativ
A:Reference number: A58811; MUID:97067211; PMID:8910613
A:Contents: annotation
R:Liljnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.

Biochemistry 37, 4699-4702, 1998
A>Title: Generation of an angiotensin-like fragment from plasminogen by streptolysin-1 (M
A:Reference number: A58812; MUID:9548733; PMID:9548733
A:Contents: annotation
R:Tulinsky, A.; Mulichak, A.M.
submitted to the Brookhaven Protein Data Bank, July 1991
A:Reference number: A51341; PDB:1PK4
A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
R:Tulinsky, A.; Wu, T.P.
submitted to the Brookhaven Protein Data Bank, July 1991
A:Reference number: A51488; PDB:2PK4
A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
R:Wu, T.P.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, August 1993
A:Reference number: A51911; PDB:1PKR
A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
R:Padmanabhan, K.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, April 1994
A:Reference number: A52408; PDB:1PMK
A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
R:Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A65244; PDB:1CEA
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R:Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A65245; PDB:1CEB
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R:Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A>Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 Å
A:Reference number: A58819; MUID:92031502; PMID:1657148
A:Contents: annotation
R:Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A>Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmin
A:Reference number: A58818; MUID:92031503; PMID:1657149
A:Contents: annotation
R:de Vos, A.M.; Ullrich, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.I
Biochemistry 31, 270-279, 1992
A>Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4
A:Reference number: A59483; MUID:92118603; PMID:1310033
A:Contents: annotation; X-ray crystallography, 2.4 angstroms
R:Stec, B.; Teetler, M.M.; Whitlow, M.; Yamano, A.
submitted to the Brookhaven Protein Data Bank, June 1995
A:Reference number: A65980; PDB:1KRN
A:Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
R:Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65803; PDB:1HPJ
A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
R:Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
R:Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A>Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
A:Reference number: 843645; MUID:94237157; PMID:8181475
A:Contents: annotation; conformation by (1)H-NMR, residues 96-184
R:Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A>Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminoge
A:Reference number: A58817; MUID:94237158; PMID:8181476
A:Contents: annotation; conformation by (1)H-NMR
C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many oth
C:Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU ar
C:Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITRU42) immediately aft
C:Comment: Microplasmin is formed by autocatalytic cleavage of plasmin under artificial condi
C:Comment: Streptolysin 1 (see PIR:KCHU51) acts on plasminogen to produce angiotensin. Tog
ting solid tumors.

C:Genetics:
 A:Gene: GDB:PLG
 A:Cross-references: GDB:119498; OMIM:173350
 A:Map position: 6q26-6q27
 A:Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529
 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a
 ne the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology
 C:Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPR>
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-810/Product: plasminogen #status experimental <PRO>
 F:20-96/Domain: activation peptide #status experimental <APT>
 F:79-466/Product: angiotensin #status experimental <AST>
 F:97-580, 581-810/Product: plasmin #status experimental <MAT>
 F:97-580/Domain: plasmin chain A #status experimental <CHA>
 F:103-181/Domain: kringe homology <KR1>
 F:185-262/Domain: kringe homology <KR2>
 F:275-352/Domain: kringe homology <KR3>
 F:377-454/Domain: kringe homology <KR4>
 F:481-560/Domain: kringe homology <KR5>
 F:550-580, 581-810/Product: microplasma #status experimental <MMT>

Query Match 11.6%; Score 359.5; DB 1; Length 810;
 Best Local Similarity 33.8%; Pred. No. 1.6e-17;
 Matches 95; Conservative 39; Mismatches 104; Indels 43; Gaps 13;

QY 23 LYDFCIV--CITTYAINVSLMMLSPKQVEPOGKAR-HGNVY-----PGEMPQASR 73
 Db 551 LDYCVPOCAAP-----SF-DGGRPOVEPKKCGRRVGGCVAPHSPWQVSAR 599
 QY 74 -RQGAHICGSLVADTWLTAACFEKAATELNSWVLSLOREGSLPGAEEVVAL 132
 Db 600 TRFGMHFCGTLSPWVLTAAHCELEKSRP--SVKVLGAQHGVNLEPHQVEIVSL 657
 QY 133 QLPRAVNHYSQGSDDLALQLAHPTHT---PLCLPQPAHRFPFGASCWATGM--DQDTS 186
 Db 658 FLE-----PTRKDILALKLSTSPAVITDKVIPACLPSPVNVADVTRCFTTGGETGTGTF 711
 QY 187 DAPGTIRNRLRLISPTNCINQHLNHPARPMLCGPQGVGPGCGSDSGGV 246
 Db 712 GA-GLKEAQLPTEIKVCN-----RYEFLNRVSTELCAGHLAGTDSGCGSGPL 764
 QY 247 LCLEPGHWQAGIISFASCAQEDAPVLLTNTAAHSSWLO 287
 Db 765 VCEPKDKYILQ-GVTSWGLGCAIRPNCVYVVRVSRVTWIE 804

RESULT 8
 146260
 plasmin (EC 3.4.21.7) precursor - western European hedgehog
 C:Species: Erinaceus europaeus (western European hedgehog)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C:Accession: I46260
 J:Lawm, R.M.; Boomark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong
 R. Biol. Chem. 270, 24004-24009, 1995
 A:Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot
 A:Reference number: I46259; MUID:96025778; PMID:7592597
 A:Accession: I46260
 A:Molecule type: mRNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-810 <LAW>
 A:Cross-references: EMBL:U03171; NID:g1046360; PID:g1046361
 C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology
 C:Keywords: hydrolase; serine proteinase
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPR>
 F:103-181/Domain: kringe homology <KR1>
 F:185-262/Domain: kringe homology <KR2>
 F:275-352/Domain: kringe homology <KR3>
 F:377-456/Domain: kringe homology <KR4>
 F:482-561/Domain: kringe homology <KR5>

F:582-803/Domain: trypsin homology <TRY>

Query Match 11.6%; Score 359; DB 2; Length 810;
 Best Local Similarity 32.8%; Pred. No. 1.8e-17;
 Matches 90; Conservative 42; Mismatches 112; Indels 30; Gaps 10;

QY 23 LYDFCIV--CITTYAINVSLMMLSPKQVEPOGKARHNTY--PGEMPQASVROGSH 78
 Db 552 LDYCDIPHCVPSSADCG-----KPKVEPKKCGRRVGGCVAPHSPWQVSLRFFGH 605
 QY 79 ICSGSLVADTWLTAACFEKAATELNSWVLSLOREGSLPGAEEVVALQPRAY 138
 Db 606 FCGGTLSPWVLTAAHCELEKSNPAI--YKVLGAHQETRLERDVQIKGVTKMFL-EX 662
 QY 133 NHYSQGSDDLALQLAHPTHT---PLCLPQPAHRFPFGASCWATGMDDTSD-APGTLR 193
 Db 663 R-----ADIALTKLSSPAITTDKDPACLPNSNVWVADRLCYITGWEETKGTYGAGLLK 717
 QY 194 NLRLLISPTNCINQHLNHPARPMLCGPQGVGPGCGSDSGGVLCLEPFG 253
 Db 718 EAQLPVIENKVCN-----RQSLNGRVSTELCAGHLAGVDSGCGSGGLVCFEKDR 771
 QY 254 HWQAGIISFASCAQEDAPVLLTNTAAHSSWLO 287
 Db 772 YILQ-GVTSWGLGCAIRPNCVYVVRVSRVSWLO 804

RESULT 9
 PLBO
 plasmin (EC 3.4.21.7) precursor - bovine
 A:Alternate names: plasminogen
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1987 #sequence_revision 28-Apr-1995 #text_change 18-Jun-1999
 C:Accession: S45046; A25835; I45961; S03736
 R:Berlund, L.; Andersen, M.D.; Petersen, T.E.
 submitted to the EMBL Data Library, May 1994
 A:Description: Cloning and characterization of the bovine plasminogen cDNA.
 A:Reference number: S45046
 A:Accession: S45046
 A:Molecule type: mRNA
 A:Residues: 1-812 <BER>
 A:Cross-references: EMBL:X79402; NID:g494962; PIDN:CA55939.1; PID:g494963
 A:Experimental source: liver
 A:Note: It is uncertain whether Met-1 or Met-8 is the initiator
 R:Schaller, J.; Moser, P.W.; Danneberger-Muller, G.A.K.; Rosselet, S.J.; Kamper, U.; Rick
 Eur. J. Biochem. 149, 267-278, 1985
 A:Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasm
 A:Reference number: A25835; MUID:85203906; PMID:3846532
 A:Accession: A25835
 A:Molecule type: protein
 A:Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
 R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
 Biochemistry 23, 4243-4250, 1984
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and t
 A:Reference number: I45961; MUID:85023311; PMID:6148961
 A:Accession: I45961
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 706-743, 'R', 745-812 <MAL>
 A:Cross-references: GB:X02935; NID:g163551; PIDN:AAA0714.1; PID:g163552
 R:Brundish, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
 Eur. J. Biochem. 114, 465-470, 1981
 A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human, t
 A:Reference number: S03735; MUID:81212097; PMID:7238497
 A:Accession: S03736
 A:Molecule type: protein
 A:Residues: 27-83 <BRU>
 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen acti
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology
 C:Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringe; plasma;

F:1-26/Domain: signal sequence #status predicted <SIG>
F:8-103/Domain: plasminogen-related protein precursor homology <PUHP>
F:27-812/Product: plasminogen #status experimental <PRO>
F:27-103/Domain: activation peptide #status experimental <APT>
F:104-583,584-812/Product: plasmin #status experimental <MAT>
F:104-583/Domain: plasmin chain A #status experimental <ACH>
F:110-188/Domain: kringle homology <KR1>
F:192-269/Domain: kringle homology <KR2>
F:282-359/Domain: kringle homology <KR3>
F:384-461/Domain: kringle homology <KR4>
F:485-564/Domain: kringle homology <KR5>
F:584-812/Domain: plasmin chain B #status experimental <BCH>
F:58-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,33
bonds: #status predicted
F:315/Binding site: carbohydrate (asn) (covalent) #status experimental
F:315/Binding site: carbohydrate (ser) (covalent) #status experimental
F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 11.5%; Score 356.5; DB 1; Length 812;
Best Local Similarity 30.8%; Pred. No. 2.7e-17;
Matches 84; Conservative 46; Mismatches 112; Indels 31; Gaps 10;

QY 24 YDFCTV--CITTYAINSLMISFRKVOEPQKAKRHNTV--PQEWQASVRRQAGHI 79
DB 556 FDYCVPOCESFDCGK-----KVEPKKCGSIVGCVSKPSWPOVSLRSSRHF 608
QY 80 CSGSLVADTWVLTAAHCEKAATELNSWSVVLGSLQREGSLPGAEVGVALLQPRAYN 139
DB 609 CGGTILSRKWLTAAHCDNLIA--LSFRKVLGHANEKVRQSOVETLPS-----RLFR 661
QY 140 HYSQGSDDLALQLAHPTHT---PLCLPQAPARPPFGASCWATGMDQDTPD-APGTURN 194
DB 662 EPSQ-ADIALKLSPALITTEKIVIPACLPPEVYVVAARPEVITGMEHQGFEGGLKE 720
QY 195 LRLRLISPTNCICINQHLNSPARPMLCGSPQPVGSPCCGDSGPPVLCLEPDGH 254
DB 721 ARLPIYENKVCN-----RNEYLDGRVKTETLCAHLLIGTDSGCGDSGPPVLCFEKXY 774
QY 255 WVQAGIISFASCAQEDAPVLLTNTAAHSSWLD 287
DB 775 ILQ-GVTSWGLGCAKPRKPGVYRVSPYVWIE 806

RESULT 10

A1545
plasmin (EC 3.4.21.7) precursor - horse (fragments)
N:Alternate names: plasminogen
N:Contains: miniplasminogen
C:Species: Equus caballus (domestic horse)
C:Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C:Accession: A61545; S17527
R:Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A:Title: Structural aspects of the plasminogen of various species.
A:Reference number: A61545; MUID:89005015; PMID:3168975
A:Accession: A61545
A:Molecule type: protein
A:Residues: 1-33;34-117 <SCH>
R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 4, 69-74, 1991
A:Title: Complete amino acid sequence of equine miniplasminogen.
A:Reference number: S17527; MUID:92052077; PMID:1946332
A:Accession: S17527
A:Molecule type: protein
A:Residues: 118-455 <SC2>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: fibrinolysis; glycoprotein; hydrolysis; kringle; plasma; serine proteinase; z
F:1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <PRO>
F:1-33/Domain: activation peptide (fragment) #status experimental <APT>
F:34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <MAT>
F:37-114/Domain: kringle homology <KR4>
F:118-455/Product: miniplasminogen #status experimental <MIN>

F:126-205/Domain: kringle homology <KR5>
F:226-445/Domain: plasmin chain B #status experimental <BCH>
F:226-448/Domain: trypsin homology <TRY>
F:267,310,405/Active site: His, Asp, Ser #status predicted

Query Match 11.4%; Score 355.5; DB 2; Length 455;
Best Local Similarity 31.5%; Pred. No. 1.6e-17;
Matches 93; Conservative 47; Mismatches 92; Indels 63; Gaps 12;

QY 23 LYDFCTVITTYAINSLMISFRKVOEPQ-----GKAKRH-----GNTVPQ----- 64
DB 196 LFDYDV-----PQESSFDCGKXVEPKKCGSIVGCVVIA 234
QY 65 -EWPQASVR-ROGAHICGSLVADTWVLTAAHCEKAATELNSWSVVLGSLQREGSLP 122
DB 235 HSWPQISLRRFGHFCGTLISPEWLTAAHCLERSRP--STYKVLGTHHELRLLAA 292
QY 123 GAEEVGVALLQPRAYNHSQGSDDLALQLAHPTHT---PLCLPQAPARPPFGASCMA 178
DB 293 GAQOIVSKFLPE-----PSRADIALKLSSPALITTONVLPACLPADYVVAWNAECFV 346
QY 179 TGM--DQDTPAPGTLRLRLISPTNCICINQHLNSPARPMLCGSPQPVGQ 236
DB 347 TGMGTQSSNA-GVLKAQLPIYENKVCN-----RIEYLNKRVKSTELCGHLVGVD 399
QY 237 PCQDGGSPVLCLEPDGHVWQAGIISFASCAQEDAPVLLTNTAAHSSWLDQARVQ 291
DB 400 SCQDGGSPVLCFEKDKYILQ-GVTSWGLGCAKPRKPGVYRVSPYVWIEIMQ 453

RESULT 11

S00845
hepsin (EC 3.4.21.-) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
C:Accession: S00845
R:leytus, S.P.; Loeb, K.R.; Hagen, F.S.; Kurachi, K.; Davie, E.W.
Biochemistry 27, 1067-1074, 1988
A:Title: A novel trypsin-like serine protease (hepsin) with a putative transmembrane dom
A:Reference number: S00845; MUID:88209431; PMID:2835076

A:Accession: S00845
A:Molecule type: mRNA
A:Residues: 1-417 <LEY>
A:Cross-references: EMBL:X07732; NID:g32063; PIDN:CAA30558.1; PID:g32064
A:Gene: GDB:HPN; TMPSL1; hepsin
A:Cross-references: GDB:135685; OMTM:142440
A:Map position: 19q11-19q13.2
C:Superfamily: hepsin; trypsin homology
C:Keywords: hydrolase; liver; serine proteinase; transmembrane protein
F:23-45/Domain: transmembrane #status predicted <TMN>
F:163-400/Domain: trypsin homology <TRY>
F:188-204,291-359,322-338,349-381/Dsulfide bonds: #status predicted
F:203,257,353/Active site: His, Asp, Ser #status predicted

Query Match 11.4%; Score 353; DB 1; Length 417;
Best Local Similarity 35.0%; Pred. No. 2.2e-17;
Matches 85; Conservative 32; Mismatches 100; Indels 26; Gaps 10;

QY 60 NTPGEWQASVRRQAGHICGSLVADTWVLTAAHCEKAATELNSWSVVLGSLQREG 119
DB 168 DTSLGRMPQOVSLRYDGAHLGSGSLISGDWVLTAAHCFERRRV-LSRRVPAQAVAO-- 224
QY 120 LSPGAEEVGVALL-----QLP-RAYNHSQGSDDLALQLAHPTHT---PLCLPQAPAR 169
DB 225 ASPHGLQGVQAVVHVGGVLPFRDPSSENSNDIALVHLSPLPLEYIQVCLPACAGA 284
QY 170 PFGASCWATGM--DQDTPAPGTLRLRLISPTNCICINQHLNSPARPMLC 227
DB 285 LVDGKICTYTGKGNQYVGGQAGVLOEARVPIISDVCH-----GADFYGQIRPKMFC 338
QY 228 GG-PQGVQGPCQDGGSPVLC--LEPDGHVWQAGIISFASCAQEDAPVLLTNTAAHS 283

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Db      339 ACYPGCGIDA-CQGSNGCFVCEDSISRPRLCGISVWGTGALQKRPVYTKVSDPR 397
QY      284 SWL 286
      398 EWI 400

RESULT 12
B30848
plasmin (EC 3.4.21.7) precursor - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #ext_change 22-Jun-1999
C:Accession: B32869; B30848
R:Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A:Reference number: A38869; MUID:89174660; PMID:2925643
A:Accession: B32869
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-810 <TOM>
A:Cross-references: GB:J04697; NID:9342272; PID:AAA6901.1; PID:9342273
C:Superfamily: plasmin, kringe homology; plasminogen-related protein precursor homology
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringe; serine proteinase
F:1-96/Domain: signal sequence #status predicted <SIG>
F:1-103/Domain: kringe homology <KR1>
F:185-262/Domain: kringe homology <KR2>
F:275-352/Domain: kringe homology <KR3>
F:377-454/Domain: kringe homology <KR4>
F:481-560/Domain: kringe homology <KR5>
F:581-803/Domain: trypsin homology <TRY>
F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
bonds: #status predicted
F:622,665,760/Active site: His, Asp, Ser #status predicted

Query Match      11.3%; Score 351.5; DB 2; Length 810;
Best Local Similarity 32.5%; Pred. No. 5,9e-17;
Matches 92; Conservative 45; Mismatches 99; Indels 47; Gaps 14;

QY      23 LVDPCIV--CITTYAINVSLMVLSPFKVQEPQCKAKR-HGNVY-----PGEMPMQASR 73
      551 LFDYCDVPCQAA-----SF-DGKRPVEPKKCPGRVVGCVAYPHSPWQISLR 599
      74 -RQSAHICGSLVADTWLTTAAHCFEKAATELNSVVLGSLQREGSLPGAEVVAL 132
      600 TLGCHHFCGGLTSPWVLTAAHCELEKSRPSF--YKVLGAREVHLERPHQIEIVSK 657
      133 QLPRAVNHYSQ--GSDLLALQLAHPHTHT---PLCLPQPAHRFPFGASCMAWGM--DD 184
      658 -----FSEPARADIALKLSSPAIITDKVIPACLPSPNVVADRTCEFTGMGETG 709
      185 TSDAPETLNLRLISRTFCNCIVQLHQRHLSNARSGMLCGGPGVQPGCCQDSG 244
      710 TGA-GLLEEARLPVLENKVCN-----RYEFLNGTVKTELCAGLACGTDSCQDSG 762
      245 PVLCLPPDGHVWQAGISFASSCAQEDAPVLTNTAHSMD 287
      763 PLVCEPKDKITLD-GVTSGLGCAKPNKGVYRVSRPTWIE 804

RESULT 13
S00657
apolipoprotein(a) (EC 3.4.21.-) precursor (validated) - human
N:Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #ext_change 08-Dec-2000
C:Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286
R:McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Bacon, D.L.; Chen, E.Y.; Fless, G.M.; Scan
Nature 330, 132-137, 1987
A:Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
A:Reference number: S00657; MUID:88039109; PMID:3670400
A:Accession: S00657

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A:Molecule type: mRNA
A:Residues: 1-4548 <MCL>
A:Cross-references: GB:X06290; EMBL:X06696; NID:928619; PID:CAA29618.1; PID:928620
R:Bacon, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.;
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A:Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to
A:Reference number: A28017; MUID:87204109; PMID:3472206
A:Accession: A28017
A:Molecule type: protein
A:Residues: 20-21,'P',23-34,177-179,'N',181-186,'T',188-196,'DKG',200,292-314,'W',316-318
X',4396-4401 <EXT>
R:Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Schwartz, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A:Title: 5' control regions of the apolipoprotein(a) gene and members of the related plas
A:Reference number: A47277; MUID:93165698; PMID:7679504
A:Accession: A47277
A:Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:L07899; NID:9967973; PID:9967974
R:Malgaroli, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Saccor
Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A:Title: Characterization by yeast artificial chromosome cloning of the linked apolipop
A:Reference number: A47233; MUID:93087573; PMID:1454851
A:Accession: I60906
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RE2>
A:Cross-references: GB:M90078; NID:9178786; PID:AAA35547.1; PID:9553188
A:Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: A47233
A:Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RE5>
A:Cross-references: GB:M90079; NID:9178784; PID:AAA35546.1; PID:9553187
R:Richnoe, A.
Biochemistry 31, 3113-3118, 1992
A:Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated wit
A:Reference number: I52415; MUID:92207924; PMID:1554698
A:Accession: I52415
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RE3>
A:Cross-references: GB:M86877; NID:9178780; PID:AA849909.1; PID:9553185
A:Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: I65286
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RE4>
A:Cross-references: GB:M86878; NID:9178782; PID:AAA51749.1; PID:9553186
C:Genetics:
A:Gene: GDB:LPA
A:Cross-references: GDB:120699; OMIM:152200
A:Map position: 6q26-q27
A:Note: several genes closely linked on chromosome 6 are identical in the first coding ex
rs of kringe repeats
C:Superfamily: apolipoprotein(a); kringe homology; trypsin homology
C:Keywords: hydrolase; kringe; lipid binding; lipoprotein; serine proteinase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-4548/Product: apolipoprotein(a) #status experimental <MAT>
F:28-105/Domain: kringe homology <KR1>
F:142-219/Domain: kringe homology <KR2>
F:256-333/Domain: kringe homology <KR3>
F:370-447/Domain: kringe homology <KR4>
F:484-561/Domain: kringe homology <KR5>
F:598-675/Domain: kringe homology <KR6>
F:712-789/Domain: kringe homology <KR7>
F:826-903/Domain: kringe homology <KR8>
F:940-1017/Domain: kringe homology <KR9>
F:1054-1131/Domain: kringe homology <KR10>
F:1168-1245/Domain: kringe homology <KR11>
F:1282-1359/Domain: kringe homology <KR12>
F:1396-1473/Domain: kringe homology <KR13>

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F:1510-1587/Domain: kringle homology <KR14>
F:1624-1701/Domain: kringle homology <KR15>
F:1738-1815/Domain: kringle homology <KR16>
F:1852-1929/Domain: kringle homology <KR17>
F:1966-2043/Domain: kringle homology <KR18>
F:2080-2157/Domain: kringle homology <KR19>
F:2194-2271/Domain: kringle homology <KR20>
F:2308-2385/Domain: kringle homology <KR21>
F:2422-2499/Domain: kringle homology <KR22>
F:2536-2613/Domain: kringle homology <KR23>
F:2650-2727/Domain: kringle homology <KR24>
F:2764-2841/Domain: kringle homology <KR25>
F:2878-2955/Domain: kringle homology <KR26>
F:2992-3069/Domain: kringle homology <KR27>
F:3106-3183/Domain: kringle homology <KR28>
F:3220-3297/Domain: kringle homology <KR29>
F:3334-3411/Domain: kringle homology <KR30>
F:3448-3525/Domain: kringle homology <KR31>
F:3562-3639/Domain: kringle homology <KR32>
F:3676-3753/Domain: kringle homology <KR33>
F:3782-3859/Domain: kringle homology <KR34>
F:3896-3973/Domain: kringle homology <KR35>
F:4010-4087/Domain: kringle homology <KR36>
F:4124-4201/Domain: kringle homology <KR37>
F:4228-4307/Domain: kringle homology <KR38>
F:4328-4541/Domain: trypsin homology <TRY>

Query Match 11.0%; Score 342; DB 1; Length 4548;

Best Local Similarity 29.4%; Pred. No. 2e-15;

Matches 83; Conservative 50; Mismatches 103; Indels 46; Gaps 10;

OY 23 LYDFCIVCITTYAINVSLMWLSFRKVOBPOGAKKHGNTV-----PGEWPMQASVR-R 74
Db 4298 LFDVC-----DIPLCASSFDGCKRPQVEPKPCPSIVGGVAHPHSPWQVSLRTR 4348
OY 75 QCAHICGSLVADTVLTAHCFEAAATELNSGVVLGSLQREGLSPGAEVGAALQL 134
Db 4349 FGKHCQGGTLLSPFWLTAHCLTKSSRP--SSYKVIILGAHVEVLESHVOEIEVSRLFL 4406
OY 135 PRAYNHYSGSLALLQLAHPTHT-----PLCLPQPARHFRPGASCMAQMDQDSD-AP 189
Db 4407 EPTQ-----ADIALKLKSRPVITDKWMPACLPSDPMVMTARTCYITGMGTGTGT 4460
OY 190 GTLRNLRLRLSRPTCNICYNOLHRLSNPARPGLCGSPQGVQCPQCGDGGPVLC 249
Db 4461 GLTKAQLLVLENVCN-HYKICAEHLARGT-----DSCQDGGSGPVLVCF 4505
OY 250 EPDGHVQAGIISFASCAQEDAPVLLNTAAHSSWLDQARVQ 291
Db 4506 EKDKYILQ-GVTSWGLGCAKRPKPGVYARVSRFTWIEGMMR 4546

RESULT 14

A2869
Apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C>Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 22-Jun-1999
C:Accession: A32869; A30848
R:Tominson, J.B.; McLean, U.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A:Reference number: A32869; PMID:89174660; PMID:2925643
A:Accession: A32869
A:Molecule type: mRNA
A:Residues: 1-1420 <TOM>
A:Cross-References: GB:J04635; NID:G342072; PID:AAA6833.1; PID:G342073
C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C:Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F:50-127/Domain: kringle homology <KR1>
F:164-241/Domain: kringle homology <KR2>
F:278-355/Domain: kringle homology <KR3>
F:392-469/Domain: kringle homology <KR4>
F:506-583/Domain: kringle homology <KR5>

F:620-697/Domain: kringle homology <KR6>
F:726-803/Domain: kringle homology <KR7>
F:840-917/Domain: kringle homology <KR8>
F:954-1031/Domain: kringle homology <KR9>
F:1068-1145/Domain: kringle homology <KR10>
F:1191-1413/Domain: trypsin homology <TRY>

Query Match 10.9%; Score 339; DB 2; Length 1420;

Best Local Similarity 32.5%; Pred. No. 8.5e-16;

Matches 82; Conservative 40; Mismatches 100; Indels 30; Gaps 9;

OY 50 EPQKAKRHGNTV-----PGEWPMQASVR-ROGAHICGSLVADTVLTAHCFEKA 101
Db 1179 KPQVEPKPCPSIVGGVAHPHSPWQVSLRTRGKFCGGLTLLSPWVLTAACTLRTFS 1238
OY 102 ATELNSMVLVGLQREGLSPGAEVGAALQLPRAVNHVSOGSDLLQLAHPTHT- 159
Db 1239 RPSF--KVILGAHQEVNLSHVOEIVSRFLFEP-----GADIALKLSPRAIITDK 1290
OY 160 --PLCLPQPARHFRPGASCWATGN--DQDTSDAPTLRNLRLSLRPTCNICYNOLH 215
Db 1291 VIPACLPSPNVITAMTECYITGMGTGTGFGA-GLTKAQLHVIENTVCN-----HYE 1343
OY 216 HLSNPARPMLCGSPQGVQCPQCGDGGSPVLCLEPQGHVQAGIISFASCAQEDAPV 275
Db 1344 FLNGRVSTELCAGHLAGTDRCOGDNGPVCDFDK-KYILRGITSWGPGACAPKRGV 1402
OY 276 LTNFAHSSWLDQ 287
Db 1403 YRVSSFTWIE 1414

RESULT 15

B61545
plasmin (EC 3.4.21.7) precursor - sheep (fragments)

N:Alternate names: plasminogen

N:Contents: miniplasminogen

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999

C:Accession: B61545; S28200

R:Schaller, J.; Rickli, E.E.

Enzyme 40, 63-69, 1988

A:Title: Structural aspects of the plasminogen of various species.

A:Reference number: A61545; PMID:8905015; PMID:3168975

A:Accession: B61545

A:Molecule type: protein

A:Residues: 1-37,38-117 <SCH>

R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.

Protein Seq. Data Anal. 5, 21-25, 1992

A:Title: Complete amino acid sequence of ovine miniplasminogen.

A:Reference number: S28200; PMID:9314995; PMID:1492092

A:Accession: S28200

A:Molecule type: protein

A:Residues: 118-460 <SC2>

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; zym

F:1-37,38-117,118-460/Product: plasminogen (fragments) #status experimental <PRO>

F:11-37/Domain: activation peptide (fragment) #status experimental <APT>

F:38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT>

F:118-460/Product: miniplasminogen <SC2>

F:141-118/Domain: kringle homology <KR4>

F:118-460/Product: miniplasminogen <status experimental <MIN>

F:132-211/Domain: kringle homology <KR5>

F:226-460/Domain: plasmin chain B #status experimental <BCH>

F:231-453/Domain: trypsin homology <TRY>

F:272,315,410/Active site: His, Asp, Ser #status predicted

Query Match 10.9%; Score 338; DB 2; Length 460;

Best Local Similarity 29.8%; Pred. No. 2.8e-16;

Matches 82; Conservative 47; Mismatches 114; Indels 32; Gaps 10;

OY 23 LYDFCIVCITTYAINVSLMWLSFRKVOBPOGAKKHGNTV--PGEWPMQASVRQO-A 77
Db 202 LFDYCDIPCCSSFDGCKP-----KVEPKCPARVVGCVATPHSPWQVSLRTRRSRE 254

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2004, 10:02:42 ; Search time 37 Seconds
(without alignments)
3096.382 Million cell updates/sec

Title: US-09-978-194a-132

Perfect score: 3108
Sequence: 1 MLSSVLVSLAGSVLAWLF.....PEPEAPGSCIANISQPTSC 571

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3108	100.0	571	10	US-09-978-697-132
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16	3108	100.0	571	11	US-09-978-193A-132	Sequence 132, App
17	3108	100.0	571	11	US-09-999-830A-132	Sequence 132, App
18	3108	100.0	571	11	US-09-978-157A-132	Sequence 132, App
19	3108	100.0	571	11	US-09-978-187B-132	Sequence 132, App
20	3108	100.0	571	11	US-09-978-643A-132	Sequence 132, App
21	3108	100.0	571	12	US-09-978-375A-132	Sequence 132, App
22	3108	100.0	571	12	US-09-978-188A-132	Sequence 132, App
23	3108	100.0	571	12	US-09-978-298A-132	Sequence 132, App
24	3108	100.0	571	12	US-10-143-031A-132	Sequence 132, App
25	3108	100.0	571	12	US-10-002-967A-132	Sequence 132, App
26	3108	100.0	571	12	US-10-017-083A-132	Sequence 132, App
27	3108	100.0	571	12	US-10-143-030A-132	Sequence 132, App
28	3108	100.0	571	12	US-10-145-128A-132	Sequence 132, App
29	3108	100.0	571	12	US-10-017-191A-132	Sequence 132, App
30	3108	100.0	571	12	US-10-143-028A-132	Sequence 132, App
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34	3108	100.0	571	12	US-10-145-017A-132	Sequence 132, App
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45	3108	100.0	571	12	US-10-145-087A-132	Sequence 132, App

ALIGNMENTS

RESULT 1
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; Sequence 132, Application US/09978295A
; Patent No. US20020156006A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertelsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Klavain, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978, 295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585

1 PRIOR FILING DATE: 1998-05-13
 2 PRIOR APPLICATION NUMBER: 60/085323
 3 PRIOR FILING DATE: 1998-05-13
 4 PRIOR APPLICATION NUMBER: 60/085582
 5 PRIOR FILING DATE: 1998-05-15
 6 PRIOR APPLICATION NUMBER: 60/085700
 7 PRIOR FILING DATE: 1998-05-15
 8 PRIOR APPLICATION NUMBER: 60/085689
 9 PRIOR FILING DATE: 1998-05-15
 10 PRIOR APPLICATION NUMBER: 60/085579
 11 PRIOR FILING DATE: 1998-05-15
 12 PRIOR APPLICATION NUMBER: 60/085580
 13 PRIOR FILING DATE: 1998-05-15
 14 PRIOR APPLICATION NUMBER: 60/085573
 15 PRIOR FILING DATE: 1998-05-15
 16 PRIOR APPLICATION NUMBER: 60/085704
 17 PRIOR FILING DATE: 1998-05-15
 18 PRIOR APPLICATION NUMBER: 60/085697

QY	1	MLSSLSVSLAGSVYLAAMLFLFVLDYFCIVCTITTYAINSLMWLSRKKVOEPQKXKHGN	60
Db	1	MLSSLSVSLAGSVYLAAMLFLFVLDYFCIVCTITTYAINSLMWLSRKKVOEPQKXKHGN	60
QY	61	TVPGEMPWQASVRRQGAHICSGSLVADWTWVLTAAHCFEKAATELNSVSVLGSIQREGI	120
Db	61	TVPGEMPWQASVRRQGAHICSGSLVADWTWVLTAAHCFEKAATELNSVSVLGSIQREGI	120
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Db	121	SPGAEFVGVAAQLPRAVNHYSGQSDLAALLQAHPTTHTPLCLPPAHRFPPGASCMATG	180
QY	181	WDOOTSAPGTLRLNRLRLISRPNTNCIYNOLHORNLPNAPRGMLCGGPQPGVQPCGG	240
Db	181	WDOOTSAPGTLRLNRLRLISRPNTNCIYNOLHORNLPNAPRGMLCGGPQPGVQPCGG	240
QY	241	DSGGPVLCLFBDGHMVQAGIISFASCSAQOEDAPVLLTJTTAAHSSMWLOARVQGAETLAQSP	300
Db	241	DSGGPVLCLFBDGHMVQAGIISFASCSAQOEDAPVLLTJTTAAHSSMWLOARVQGAETLAQSP	300
QY	301	ETPEMSDEDCSVACGSLRTAGBQAGAPSPWPEEARLHMGOGLACGALVSEBAVLTAAHC	360
Db	301	ETPEMSDEDCSVACGSLRTAGBQAGAPSPWPEEARLHMGOGLACGALVSEBAVLTAAHC	360
QY	361	FIGBOAPEWMSGJCTRPEEWGLKOLLIHGATTHEGGYDMLLLLAQVTTIGASIRPLC	420
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QY	421	LPYRDHHLPRDERGVLGRARPGAISSLSQTPVULLGPRACSRLLHAAPGGGSPILPBM	480
Db	421	LPYRDHHLPRDERGVLGRARPGAISSLSQTPVULLGPRACSRLLHAAPGGGSPILPBM	480
QY	481	VCTSAVGEIPLSCGELISGAPLVHEVNGTWFLAGHSFGDAGCGPARPAVFTALPAYEDWVS	540
Db	481	VCTSAVGEIPLSCGELISGAPLVHEVNGTWFLAGHSFGDAGCGPARPAVFTALPAYEDWVS	540
QY	541	SLDMQVYFAEBEPPEAPBPGSCIANISOPRSC	571
Db	541	SLDMQVYFAEBEPPEAPBPGSCIANISOPRSC	571

RESULT 2
US-09-978-697-132
Sequence 132, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc

APPLICANT: Faton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 10; Length 571;
Best Local Similarity 100.0%; Pred. No. 4,4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLSSLSVLAGSVYLAWLIFVLYNDCTVCTTAIVNINSLMWLSRKYOEPOGKAKRHN 60
QY 61 TVPGEMPQASVRRQGAHICSGSLVADTWVLTAAHCFEAAATEINSMVLSGSLQREGL 120
DB 61 TVPGEMPQASVRRQGAHICSGSLVADTWVLTAAHCFEAAATEINSMVLSGSLQREGL 120
QY 121 SPGAEEVGAALQLPRAVNHYSQGSDDLALQLAHPTHTPLCLPPAHRFPGASCMATG 180
DB 121 SPGAEEVGAALQLPRAVNHYSQGSDDLALQLAHPTHTPLCLPPAHRFPGASCMATG 180
QY 181 WQODTSDAPGTIRNRLRLISRPCTNCIYNQJHQRHLSNPAPRPGMLCGSPQGVGPPCG 240
DB 181 WQODTSDAPGTIRNRLRLISRPCTNCIYNQJHQRHLSNPAPRPGMLCGSPQGVGPPCG 240
QY 241 DSGEPVLCLEPDDGHVWQGIISFASSCAOEDAPVLLTNTAAHSSWLOARVQGAATLAOSP 300
DB 241 DSGEPVLCLEPDDGHVWQGIISFASSCAOEDAPVLLTNTAAHSSWLOARVQGAATLAOSP 300
QY 301 ETPEMSDEDSVACSGSLRTAGPQAGPSPWPWEARLMHQGLACGALVSEBAVLTAAHC 360

Db 301 ETPEMSDSDSCVACGSLTAPGQAPSPWEAKLMQGLACGALVSEAVLTAHC 360
Qy 361 FIGRAPEWESVGLTGREEMGLKOLLHGAATHEGGYDMLLLAOPVTLGASLRPLC 420
Db 361 FIGRAPEWESVGLTGREEMGLKOLLHGAATHEGGYDMLLLAOPVTLGASLRPLC 420
Qy 421 LPPDHHLPDGERGVNLGARPGAGISSLQTVPTLLGRACSRLLHAPGGDGSPIFGM 480
Db 421 LPPDHHLPDGERGVNLGARPGAGISSLQTVPTLLGRACSRLLHAPGGDGSPIFGM 480
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Db 481 VCTSAVGLPSCGSGAPLVHEVGTWFLAGHFGACCGPARPAVFTALPAEDWVS 540
Qy 541 SLDMOVFAEPEPEAPSPSCIANISOPTSC 571
Db 541 SLDMOVFAEPEPEAPSPSCIANISOPTSC 571

RESULT 3

US-09-978-192A-132
Sequence 132, Application US/09978192A
Patent No. US2002017553A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Kijavlin, Ivar J.
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James:
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
Query Match 100.0%; Score 3108; DB 10; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MLSSIVSLAGSVYLAHIFVLYDFCIYCTTYAINVSLMWLSPRKYOPQKAKRHGN 60
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61 TVPGWPMQASVRRQCAHICSGSLVADTWLTLAHCFEKAAATELNSWSVLGSLQREGL 120
Db 61 TVPGWPMQASVRRQCAHICSGSLVADTWLTLAHCFEKAAATELNSWSVLGSLQREGL 120
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Db 301 ETPEMSDEDSVCACSLRTRAGQAPSPWPEALHMOGOLACGALVSEAVLTLAHC 360
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QY 541 SUDMOVFAEPEPEAPSPSCIANISOPTSC 571
541 SUDMOVFAEPEPEAPSPSCIANISOPTSC 571
Db 541 SUDMOVFAEPEPEAPSPSCIANISOPTSC 571
RESULT 4
US-09-999-832A-132
Sequence 132, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/078004
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PRIOR FILING DATE: 1998-04-01

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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
 Best Local Similarity 100.0%; Pred. No. 4,4e-245; Indels 0; Gaps 0;
 Matches 571; Conservative 0; Mismatches 0;

QY 1 MLSSIVSLAGSVLAWILFFVLVDPCITTYAINVSLMWLSFRKVOEPOGAKRRGN 60
 DB 1 MLSSIVSLAGSVLAWILFFVLVDPCITTYAINVSLMWLSFRKVOEPOGAKRRGN 60
 QY 61 TVPGEMPQASVVRQGAHICGSLVADTWTWLTAAHCFEKAATELNSVSLGSLOREGL 120
 DB 61 TVPGEMPQASVVRQGAHICGSLVADTWTWLTAAHCFEKAATELNSVSLGSLOREGL 120

Qy	122	SPFAEEVGAALQLPRAVYHYSGQSDLLALQLAHPTTHTPLCLPPAPRPFPGASCMATG	1.80
Db	121	SPFAEEVGAALQLPRAVYHYSGQSDLLALQLAHPTTHTPLCLPPAPRPFPGASCMATG	1.80
Qy	181	WDQDTSDAFGTLNRLNRLISRPNCNIYNQLOHRLHNSNPARPGMLCGGPQGVGBCQG	2.40
Db	181	WDQDTSDAFGTLNRLNRLISRPNCNIYNQLOHRLHNSNPARPGMLCGGPQGVGBCQG	2.40
Qy	241	DSCGAPVLCLEPDSHWQAGIISFPASSCAQEDAPVLLTNTAAHSSMLQARVQGAFLTAOSP	3.00
Db	241	DSCGAPVLCLEPDSHWQAGIISFPASSCAQEDAPVLLTNTAAHSSMLQARVQGAFLTAOSP	3.00
Qy	301	ETPEMSDEDSCVACGSLRTACPOACAPEFMPPEARLHMQGLACGALVSEEAFLTAHC	3.60
Db	301	ETPEMSDEDSCVACGSLRTACPOACAPEFMPPEARLHMQGLACGALVSEEAFLTAHC	3.60
Qy	361	FIRQAPPEMSVGLGTRPEEMGLKOLLHGATTHEGGYDALLLLAOPVTLGASLRPLC	4.20
Db	361	FIRQAPPEMSVGLGTRPEEMGLKOLLHGATTHEGGYDALLLLAOPVTLGASLRPLC	4.20
Qy	421	LPPPDHHLPPGEGRGWLGRAPGAGISSLOTPTVLLPRACSRLLHAPGGDGSPIIPGM	4.80
Db	421	LPPPDHHLPPGEGRGWLGRAPGAGISSLOTPTVLLPRACSRLLHAPGGDGSPIIPGM	4.80
Qy	481	VCTSAVGEELPSCGELSGAPLVHEVGTWFLAGLHSGDACCOPARPAVFTALLPAYEDWVS	5.40
Db	481	VCTSAVGEELPSCGELSGAPLVHEVGTWFLAGLHSGDACCOPARPAVFTALLPAYEDWVS	5.40
Qy	541	SLDMOYVFAEPEPEPEPEPSSCLANISQPTSC	5.71
Db	541	SLDMOYVFAEPEPEPEPEPSSCLANISQPTSC	5.71

RESULT 6
US-09-978-608A-132
Sequence 132, Application US/09978608A
Publication No. US20030045462A1
GENERAL INFORMATION:
APPLICANT: Askenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Denoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC22
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ. ID NOS: 624
Prior Application removed - See File Wrapper or Palm

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; SEQ ID NO 132
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-132

Query Match          100.0%; Score 3108; DB: 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4,4e+245; Indels 0; Gaps 0
Matches 571; Conservative 0; Mismatches 0;

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QY	1	MLLSLSVLSIAGSVLWAMLLFVLVDFVCVCTTAAIVNSLMMISLFRVQOEQCAKXGN	60
Db	1	MLLSLSVLSIAGSVLWAMLLFVLVDFVCVCTTAAIVNSLMMISLFRVQOEQCAKXGN	60
QY	61	TYVGEWPMQASVVRQGAHICSGSLVADTWVLTAACEKKAATELNMSVVLGSLQREG	120
Db	61	TYVGEWPMQASVVRQGAHICSGSLVADTWVLTAACEKKAATELNMSVVLGSLQREG	120
QY	121	SPGAEVVGAAQLPRAYNHSQSGDLALLOLAHTHTPLCLPQPAHRRFGASCMATG	180
Db	121	SPGAEVVGAAQLPRAYNHSQSGDLALLOLAHTHTPLCLPQPAHRRFGASCMATG	180
QY	181	WQODTSDAGTLRNLRRLISRPTNCIYNLOHORHLSNRPGLCGGPOPGVQGCQG	240
Db	181	WQODTSDAGTLRNLRRLISRPTNCIYNLOHORHLSNRPGLCGGPOPGVQGCQG	240
QY	241	DGSGPYCLERPDMHWQAGIISFASSCAEDAPVLLNTAAHSSWLOARVQGAFLAQSP	300
Db	241	DGSGPYCLERPDMHWQAGIISFASSCAEDAPVLLNTAAHSSWLOARVQGAFLAQSP	300
QY	301	ETPEMSDEBSCVACGSLRTAGPQAGAPBPMWEKRLNHQGLACGALVSEEAULTAHNC	360
Db	301	ETPEMSDEBSCVACGSLRTAGPQAGAPBPMWEKRLNHQGLACGALVSEEAULTAHNC	360
QY	361	FTGRQAPREBMSVGLTRPEEWGLKOLLHGAYTRPEGGYDMAILLYLAQPTLIGASLRLC	420
Db	361	FTGRQAPREBMSVGLTRPEEWGLKOLLHGAYTRPEGGYDMAILLYLAQPTLIGASLRLC	420
QY	421	LPRPDHHLRDEGRGVILGRAPGAGISSLOTPVTLTGPRACSRHLHAPGSDGSPILPGM	480
Db	421	LPRPDHHLRDEGRGVILGRAPGAGISSLOTPVTLTGPRACSRHLHAPGSDGSPILPGM	480
QY	481	VCTSAVAGELPSCGEGISGAPLVHEVRGTFVLGLHSGFDACGPRAPVFTALPAYEDWVS	540
Db	481	VCTSAVAGELPSCGEGISGAPLVHEVRGTFVLGLHSGFDACGPRAPVFTALPAYEDWVS	540
QY	541	SLDMOYVFAEPEPEAPBPGSCLIANSOPTSC	571
Db	541	SLDMOYVFAEPEPEAPBPGSCLIANSOPTSC	571

RESULT 7
US-09-978-5854-132
Sequence 132, Application US/099785854
Publication No. US20030049633A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.


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? PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4,4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLTSLVSLAGSVLYLWMLFVLYDPCIVCTTTAIVNSLWMLSPRKYQEPQKAKRGN 60
DB 1 MLTSLVSLAGSVLYLWMLFVLYDPCIVCTTTAIVNSLWMLSPRKYQEPQKAKRGN 60
QY 61 TYPGEVPMQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATTELSNSVYLSIQREGL 120
DB 61 TYPGEVPMQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATTELSNSVYLSIQREGL 120
QY 121 SPGAEEVGAALQLEPRANVHSQGSDDLALLOLAHPTHTPLCLPQPARHFPFGASCWMTG 180
DB 121 SPGAEEVGAALQLEPRANVHSQGSDDLALLOLAHPTHTPLCLPQPARHFPFGASCWMTG 180
QY 181 WDQDTSAPAGTLRNLRLLISRPTCNCTYNQLHQRHLSNPARPGMLCGGPQGVGPGCG 240
DB 181 WDQDTSAPAGTLRNLRLLISRPTCNCTYNQLHQRHLSNPARPGMLCGGPQGVGPGCG 240
QY 241 DSGPVLCLPDDGHVWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAFLAOSP 300
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Db 241 DSGGVLCLEPDGHVQGIISFASSCAQEDAPVLLTNTAAHSSWLOQAVQGAATLAQSP 300
Qy 301 ETPEMSDEDSVCVACGSLFTAGPQAGAPSPWPEARLHMHQGLACGALVSEAVITAAHC 360
Db 301 ETPEMSDEDSVCVACGSLFTAGPQAGAPSPWPEARLHMHQGLACGALVSEAVITAAHC 360
Qy 361 FTGRAPAEWWSVGLGTREPEWGLKOLLHGAYTHPEBGYDMLALLAOPVTLGASLRPLC 420
Db 361 FTGRAPAEWWSVGLGTREPEWGLKOLLHGAYTHPEBGYDMLALLAOPVTLGASLRPLC 420
Qy 421 LEPYPHHLPDGERGWLGARPGAGISSQTPVTLGGRASRLHAAPGGSPILPQM 480
Db 421 LEPYPHHLPDGERGWLGARPGAGISSQTPVTLGGRASRLHAAPGGSPILPQM 480
Qy 481 VCTSAVGEIPECEGSLGAPLVHEVGTWFLAGHSFGDACQGPAPPAVFTALPAYEDWS 540
Db 481 VCTSAVGEIPECEGSLGAPLVHEVGTWFLAGHSFGDACQGPAPPAVFTALPAYEDWS 540
Qy 541 SLDMQVYFAEPEPEPEAPGSCLANISQPTSC 571
Db 541 SLDMQVYFAEPEPEPEAPGSCLANISQPTSC 571

RESULT 9

US-09-978-403A-132

Sequence 132, Application US/09978403A

Publication No. US20030050240A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Iwar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2650P17
CURRENT APPLICATION NUMBER: US/09/978, 403A
PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
 Best Local Similarity 100.0%; Pred. No. 4,4e-245;
 Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLSSLSVSLAGSVYLAAMILFVLYDFCTVCTTTAININSIMLSTRKXOEPOGKAKRGN 60
 1 MLSSLSVSLAGSVYLAAMILFVLYDFCTVCTTTAININSIMLSTRKXOEPOGKAKRGN 60
 61 TVPGEMPQASVRRQGAHICSGSLVADTWVLTAAACFEAAATELNSVSVGLSLOREGL 120
 61 TVPGEMPQASVRRQGAHICSGSLVADTWVLTAAACFEAAATELNSVSVGLSLOREGL 120
 61 TVPGEMPQASVRRQGAHICSGSLVADTWVLTAAACFEAAATELNSVSVGLSLOREGL 120
 121 SPGAEVGVAAALQLPRAYNHVSQGSDDLALQLAHPTHTPLCLPQPARHFPFGASCWATG 180
 121 SPGAEVGVAAALQLPRAYNHVSQGSDDLALQLAHPTHTPLCLPQPARHFPFGASCWATG 180
 181 WQDPTSDAPGTIRNRLRLISRPCTNCITYNQHLNPNRPMGLCGPGQVGVPCOG 240
 181 WQDPTSDAPGTIRNRLRLISRPCTNCITYNQHLNPNRPMGLCGPGQVGVPCOG 240
 241 DSGGPEVLCLEPDGHVQAGIISFASSCAOEDAPVLLTTAAHSMLOARVOGAFTLAOSP 300
 241 DSGGPEVLCLEPDGHVQAGIISFASSCAOEDAPVLLTTAAHSMLOARVOGAFTLAOSP 300
 301 ETPEMSDEDSVCAACSLRTAGPQAGAPSPWPEARLMHQGLACGALVSEBAVLTAAHC 360
 301 ETPEMSDEDSVCAACSLRTAGPQAGAPSPWPEARLMHQGLACGALVSEBAVLTAAHC 360
 361 FIGROAPEEWSVGLTREBEWGLKOLIHGAYTHEGGYDVALLLAOPVTLGASLRPLC 420
 361 FIGROAPEEWSVGLTREBEWGLKOLIHGAYTHEGGYDVALLLAOPVTLGASLRPLC 420
 421 LPYPDHHLPDGERGVNLRARPGAGISSIQVPTVLLPGRACSRJHAAPGGDGSPLPCM 480
 421 LPYPDHHLPDGERGVNLRARPGAGISSIQVPTVLLPGRACSRJHAAPGGDGSPLPCM 480
 481 VCTSAVGEIPLSCGEGSLGAPLVHEVRGTWFLAGLSFGDAPARPAVFTALPAYEDWVS 540
 481 VCTSAVGEIPLSCGEGSLGAPLVHEVRGTWFLAGLSFGDAPARPAVFTALPAYEDWVS 540
 541 SLDMQVYFAEBEPPEABEPGSCIANISOPTSC 571
 541 SLDMQVYFAEBEPPEABEPGSCIANISOPTSC 571

RESULT 10
 US-09-978-564A-132
 Sequence 132, Application US/09978564A
 Publication No. US20030050241A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Geider, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.

Query Match	100.0%	Score 3108	DB 11	Length 571
Best Local Similarity	100.0%	Pred. No. 4.4e-245		
Matches 571	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy		MLSSLSVSIASSVYLAAMIILFVLYDPCIVCTITTAIYNSIMLSIRKVOEPOGKXKHGN	60
Db	1	MLSSLSVSIASSVYLAAMIILFVLYDPCIVCTITTAIYNSIMLSIRKVOEPOGKXKHGN	60
Qy		61 TVPCEWPMQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSVVLGSLQREGI	120
Db		61 TVPCEWPMQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSVVLGSLQREGI	120
Qy		121 SPGAEVGVAAALQLPRAVNYHSQSGDMLLQLAHFTTTPLCIPQPARHFFPGASCMATG	180
Db		121 SPGAEVGVAAALQLPRAVNYHSQSGDMLLQLAHFTTTPLCIPQPARHFFPGASCMATG	180
Qy		181 WDQSTDPAGTILRNRLRLISRPPTNCITYNQLHQRLSNPARPGMLCGSPGCVGSPCCG	240
Db		181 WDQSTDPAGTILRNRLRLISRPPTNCITYNQLHQRLSNPARPGMLCGSPGCVGSPCCG	240
Qy		241 DSGGPVLCLEPBGHWVQAGIISFASSCAQEDAPVLLTNTAAHSMVLQARVQGAFLAOSP	300
Db		241 DSGGPVLCLEPBGHWVQAGIISFASSCAQEDAPVLLTNTAAHSMVLQARVQGAFLAOSP	300
Qy		301 ETPEMSDSDSCVACSLRTAGQAPABPWPMEARLMOGQLACGALVSEEAULTAAHC	360
Db		301 ETPEMSDSDSCVACSLRTAGQAPABPWPMEARLMOGQLACGALVSEEAULTAAHC	360
Qy		361 FIGRQAPPEWMSGVIGTRPEEWGLKQLLIHGATVTHEGGYDMLLLLAQPVTLGASLRPLC	420
Db		361 FIGRQAPPEWMSGVIGTRPEEWGLKQLLIHGATVTHEGGYDMLLLLAQPVTLGASLRPLC	420
Qy		421 LPYPDHHLPDQERGVNLGRAPAGAGISLQTYPVTLIGPRACSRLLHAAPGGGSPILPDM	480
Db		421 LPYPDHHLPDQERGVNLGRAPAGAGISLQTYPVTLIGPRACSRLLHAAPGGGSPILPDM	480

RESULT 11

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Sequence 132, Application US/099999833A
Publication No. US20030054405A1
GENERAL INFORMATION:
APPLICANT: Askenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kijavrin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. McKey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
 Best Local Similarity 100.0%; Pred. No. 4.4e-245;
 Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSSLSVSLAGSVYLLAMIFVLYIDPCITCTTYYAINVSLMWSLSPKVOEPQKAKRHGN 60
 DB 1 MLSSLSVSLAGSVYLLAMIFVLYIDPCITCTTYYAINVSLMWSLSPKVOEPQKAKRHGN 60

QY 61 TVPGEMPNQASVRQGAHICSGSLVADTWLTAACFEKAAATELNSWSVGLSLOREGI 120
DB 61 TVPGEMPNQASVRQGAHICSGSLVADTWLTAACFEKAAATELNSWSVGLSLOREGI 120
QY 121 SPQAEVGVAAALQPPAYNHYSGSGSLALLQALHPHTTHPLCLPOPABHPPFGASCWAG 180
DB 121 SPQAEVGVAAALQPPAYNHYSGSGSLALLQALHPHTTHPLCLPOPABHPPFGASCWAG 180
QY 181 WDDGTSADAGTJLNLRLRLISRPTCNCIYNQHLSPNRPBGMCGGPQVQPCOG 240
DB 181 WDDGTSADAGTJLNLRLRLISRPTCNCIYNQHLSPNRPBGMCGGPQVQPCOG 240
QY 241 DSGGVLCLPEPDGHWVQAGISFASSCAQEDAVLLTNAAHSSWQARQGAFLAOSP 300
DB 241 DSGGVLCLPEPDGHWVQAGISFASSCAQEDAVLLTNAAHSSWQARQGAFLAOSP 300
QY 301 ETEPMEDSCVACGSLRTAGPOAGAPSPWPWEARLMHQQLACGALVSEBAVLTAAC 360
DB 301 ETEPMEDSCVACGSLRTAGPOAGAPSPWPWEARLMHQQLACGALVSEBAVLTAAC 360
QY 361 FIGROAPEWSVGLGTRPEEMGLKQILHGAYTHPEGYDMALLLHAOPVTLGASLRPLC 420
DB 361 FIGROAPEWSVGLGTRPEEMGLKQILHGAYTHPEGYDMALLLHAOPVTLGASLRPLC 420
QY 421 LPPDHLHPDGERGWLGRAPGAGISLQTVVTLGPRACRLHAAPGDCGSPILPGN 480
DB 421 LPPDHLHPDGERGWLGRAPGAGISLQTVVTLGPRACRLHAAPGDCGSPILPGN 480
QY 481 VCTSAVAGELPSCGSLGAPVHEVRGWLFLAGHSGDQCGGARPAVFLPAYEDWS 540
DB 481 VCTSAVAGELPSCGSLGAPVHEVRGWLFLAGHSGDQCGGARPAVFLPAYEDWS 540
QY 541 SLDWQVFAEPEPEPEPEPSCLANISQPTSC 571
DB 541 SLDWQVFAEPEPEPEPEPSCLANISQPTSC 571

RESULT 12
US-09-981-915A-132
Sequence 132, Application US/09981915A
Publication No. US20030054986A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C12

CURRENT APPLICATION NUMBER: US/09/981,915A
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4,4e-245; Indels 0; Gaps 0;
Matches 571; Conservative 0; Mismatches 0;

QY 1 MLSSIVSLAGSVYLAHILFFVLDFYFCITTYAINVSLMWSFRKYOEPOGAKKHGN 60
DB 1 MLSSIVSLAGSVYLAHILFFVLDFYFCITTYAINVSLMWSFRKYOEPOGAKKHGN 60
QY 61 TVPEWMPQASVRRQGAHICGSLVADTWVITAAHCEKAATELNSVSVLSLOREG 120
DB 61 TVPEWMPQASVRRQGAHICGSLVADTWVITAAHCEKAATELNSVSVLSLOREG 120
QY 121 SPGAEEVGVAAALQIPRAVNHVSQSDLAALQIAHPTHTPLCLPOPHRPFEGSCWATG 180
DB 121 SPGAEEVGVAAALQIPRAVNHVSQSDLAALQIAHPTHTPLCLPOPHRPFEGSCWATG 180
QY 121 WDOPTSDAPGTLRLRLISRPNCIYNQLOHQRHLSNPARPMLCGGPQGVQPCOG 240
DB 121 WDOPTSDAPGTLRLRLISRPNCIYNQLOHQRHLSNPARPMLCGGPQGVQPCOG 240
QY 181 DSGGPFVLCLEPDDHVMVAGIISFASSCAQEDAPVLLNTAAHSSWLQARVGAALFLAQP 300
DB 181 DSGGPFVLCLEPDDHVMVAGIISFASSCAQEDAPVLLNTAAHSSWLQARVGAALFLAQP 300
QY 241 DSGGPFVLCLEPDDHVMVAGIISFASSCAQEDAPVLLNTAAHSSWLQARVGAALFLAQP 300
DB 241 DSGGPFVLCLEPDDHVMVAGIISFASSCAQEDAPVLLNTAAHSSWLQARVGAALFLAQP 300
QY 301 ETPEMSDESDSCVACGSILRTAGPCAGAPS PWEWEARLHQGLACGALVSEAVLTAHC 360
DB 301 ETPEMSDESDSCVACGSILRTAGPCAGAPS PWEWEARLHQGLACGALVSEAVLTAHC 360
QY 361 FIGROAPEWMSVIGTRPEEWGLKQILIHGAYTHPEGGYDMLALLAQPTVLGASLRPLC 420
DB 361 FIGROAPEWMSVIGTRPEEWGLKQILIHGAYTHPEGGYDMLALLAQPTVLGASLRPLC 420
QY 421 LPPDHLPLDGERGVMVIGRARPGAGISLSQTVPTLLGPRACSRLLHAAPGDSPIILPGM 480
DB 421 LPPDHLPLDGERGVMVIGRARPGAGISLSQTVPTLLGPRACSRLLHAAPGDSPIILPGM 480
QY 481 VCTSAVGEPLPSCEGSLGAPLVHEVRGTWFLAGLSFGDACGCGPARPAVFTALPAYEDVVS 540
DB 481 VCTSAVGEPLPSCEGSLGAPLVHEVRGTWFLAGLSFGDACGCGPARPAVFTALPAYEDVVS 540
QY 541 SLDWQVFAEERPEAPGSCLANISOPTSC 571
DB 541 SLDWQVFAEERPEAPGSCLANISOPTSC 571

RESULT 13
US-09-978-824-132
Sequence 132, Application US/09978824
Publication No. US20030055216A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Godowski, Paul J.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C14
CURRENT APPLICATION NUMBER: US/09/978,824
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;

Best Local Similarity 100.0%; Pred. No. 4,4e-245; Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLSSLSVSLAGSVYLAHIFVLYDFCIYCTTAYANVSLMMLSPKVOEPQOKAKRHN 60
1 MLSSLSVSLAGSVYLAHIFVLYDFCIYCTTAYANVSLMMLSPKVOEPQOKAKRHN 60
1 TVGGEWPMQASVYRQGAHICSGSLVADTVLTAHCFEKAATELNSWSVVLGSLQREG 120
61 TVGGEWPMQASVYRQGAHICSGSLVADTVLTAHCFEKAATELNSWSVVLGSLQREG 120
121 SPGAEEVGAALQPLPAAVHYSGSDALALLOLAHPHTHTPLCLPQAHFPPGASCMATG 180
121 SPGAEEVGAALQPLPAAVHYSGSDALALLOLAHPHTHTPLCLPQAHFPPGASCMATG 180
181 WDDTSDAGTLLRLRLISRTNCIYNOLHQRHLSNPARPGMLCGSPGPGVCGP 240
181 WDDTSDAGTLLRLRLISRTNCIYNOLHQRHLSNPARPGMLCGSPGPGVCGP 240
241 DSGGVLCLPEPDGHVQAGIISASSCAQBDPAVLLTNTAAHSSWIOARVQGAFLAOSP 300

241 DSGGVLCLPEPDGHVQAGIISASSCAQBDPAVLLTNTAAHSSWIOARVQGAFLAOSP 300
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301 ETPWSDSDSCVACGSLRTAGPQAGAPSPWPEARLHQGLACGALVSEAVLTAAC 360
361 FIGRAPEBSVGLCTREEWGLKQLIHGAYTHPEGGYDVALLLAOPVTLGASLRPLC 420
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RESULT 14
US-09-918-585A-132
Sequence 132, Application US/09918585A
Publication No. US20030060406A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/09/918, 585A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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[illegible]

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; PRIOR APPLICATION NUMBER: 60/086023
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Query Match      100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4,4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLSSVSLAGSVYLAAMLFVLYDCTICITTYAINVSLMLSFKNQVEPOGKARHN 60
QY 61 TVPGEMPQASVYRQGAHICSGSLVADTWLTPAHCFEKAATELMSVGLSLOREGI 120
DB 61 TVPGEMPQASVYRQGAHICSGSLVADTWLTPAHCFEKAATELMSVGLSLOREGI 120
QY 121 SPQAEVGVAAIQLPRAVYHYSGSDLLALLOLAHPTTHPLCLPQAHFPFGASCWATG 180
DB 121 SPQAEVGVAAIQLPRAVYHYSGSDLLALLOLAHPTTHPLCLPQAHFPFGASCWATG 180
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QY 241 DSGGPLYCLPEPDHAWQAGIISFASCAQEDAPVLLTNTAHSWQARVOGAFLAOSP 300
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QY 301 ETPREMSDEDCVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGALVSEAVLTAHC 360
DB 301 ETPREMSDEDCVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGALVSEAVLTAHC 360
QY 361 FIGRQAPPEMSVGLGTRPEWGLKQILHGAYTHPGCGIDMALLLAQPYTLGASLRPLC 420
DB 361 FIGRQAPPEMSVGLGTRPEWGLKQILHGAYTHPGCGIDMALLLAQPYTLGASLRPLC 420
QY 421 LPPYDHLDPGGERGWLGRARPGAGISSIQTVVTLGPRACRLHAAGGGSDPLIPM 480
DB 421 LPPYDHLDPGGERGWLGRARPGAGISSIQTVVTLGPRACRLHAAGGGSDPLIPM 480
QY 481 VCTSAVGEPLPSCEGLSGAPLVHEVRGTWFLAGHSFGDCCQGPAPVFTALPAYEDWYS 540
DB 481 VCTSAVGEPLPSCEGLSGAPLVHEVRGTWFLAGHSFGDCCQGPAPVFTALPAYEDWYS 540
QY 541 SLDMQVYFAEEPEPEAPGSCLANISQPTSC 571
DB 541 SLDMQVYFAEEPEPEAPGSCLANISQPTSC 571

RESULT 15
US-09-978-423A-132
; Sequence 132, Application US/09978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guirne, Austin L.
; APPLICANT: Hillen, Kenneth J
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
;
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC21
CURRENT APPLICATION NUMBER: US/09/978,423A
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
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PRIOR APPLICATION NUMBER: 60/084414
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PRIOR FILING DATE: 1998-05-06

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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: 60/085323
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PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4,4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLSSLSVLAGSVYLAHILFVLYDFCICTTVAINSLMMLSRKVOEPQKAKRGN 60
1 MLSSLSVLAGSVYLAHILFVLYDFCICTTVAINSLMMLSRKVOEPQKAKRGN 60
61 TVPGEMPQASVRRQGAHICSGSLVADTWTVAHCFFKAATELNSVVLGSIQREG 120
61 TVPGEMPQASVRRQGAHICSGSLVADTWTVAHCFFKAATELNSVVLGSIQREG 120
121 SPGAEEVGAALQLEPRAYNHISQGSDDLALQLAHPTHTPLCPAHRFPFGASCWATG 180
121 SPGAEEVGAALQLEPRAYNHISQGSDDLALQLAHPTHTPLCPAHRFPFGASCWATG 180
181 WQDPTSDAPGTLRNRLRLISPTNCIYNOLHSHLNPARGMLCGGPOPGVPCOG 240
181 WQDPTSDAPGTLRNRLRLISPTNCIYNOLHSHLNPARGMLCGGPOPGVPCOG 240
241 DSGEVLCLPEPDGHWVQAGIISFASCAQEDAPVLLTTAAHSSWLQARVQGAFLAOSP 300
241 DSGEVLCLPEPDGHWVQAGIISFASCAQEDAPVLLTTAAHSSWLQARVQGAFLAOSP 300
301 ETPEWSDSDSCVACSLRTAGPQAPSPMPWEARLMHQGLACGALVSEAVITAAHC 360
301 ETPEWSDSDSCVACSLRTAGPQAPSPMPWEARLMHQGLACGALVSEAVITAAHC 360
361 FIGRQAPPEWSVGLCTREEMWGLKLIHGAYTHEGGYDVALLLLAQPVTLGASLRPLC 420
361 FIGRQAPPEWSVGLCTREEMWGLKLIHGAYTHEGGYDVALLLLAQPVTLGASLRPLC 420
421 LPYPDHHLPDGERGVNLRARPGAGISLQTYPVTLGPRACSRHAAFGDGPSPILPGM 480
421 LPYPDHHLPDGERGVNLRARPGAGISLQTYPVTLGPRACSRHAAFGDGPSPILPGM 480
481 VCTSAVGLPSCGSLGAPLVHEVRGTWFLAGLSFGDAGCOPARPAVFTALPAYEDWS 540

Db	481	VCTSAVGBLPSCBGLGAPLVHVRGTWFLAGLHSGDACGGPARPAVFTALPAYEDWVS	540
Oy	541	SLDMQVYFAEBEPPEAEPGSCLANISQPTSC	571
Db	541	SLDMQVYFAEBEPPEAEPGSCLANISQPTSC	571

Search completed: January 6, 2004, 10:08:18
Job time : 38 secs

No.	Score	Match Length	DB	ID	Description
1	449	14.4	290	4	US-09-386-653A-7
2	447	14.4	284	4	US-09-387-375-7
3	447	14.4	316	4	US-09-387-375-9
4	446	14.4	315	4	US-09-386-653A-9
5	429.5	13.8	299	3	US-08-944-483-6
6	422	13.6	319	4	US-09-386-642-12
7	422	13.6	328	4	US-09-386-642-11
8	400	12.9	317	4	US-09-386-629-8
9	388	12.5	327	4	US-09-386-629-8
10	375	12.1	902	4	US-09-644-600-10
11	370.5	11.9	790	4	US-08-991-761A-13
12	369.5	11.9	812	1	US-08-248-629A-1
13	369.5	11.9	812	1	US-08-451-932-1
14	369.5	11.9	812	1	US-08-452-260-1
15	369.5	11.9	812	1	US-08-346-785-1
16	369.5	11.9	812	2	US-08-612-788-1
17	369.5	11.9	812	2	US-08-605-598B-1
18	369.5	11.9	812	2	US-08-429-743-1
19	369.5	11.9	812	2	US-08-866-735-1
20	369.5	11.9	812	3	US-09-066-028-1
21	369.5	11.9	812	4	US-09-192-012-3
22	369.5	11.9	812	4	US-09-335-325-1
23	369.5	11.9	812	4	US-08-991-761A-12
24	369.5	11.9	812	5	PCT-US95-05107-1
25	363.5	11.7	791	1	US-08-643-219-1
26	363.5	11.7	791	1	US-08-851-350-1
27	362.5	11.7	285	4	US-09-023-942A-26

28	361.5	11.6	855	2	US-09-027-337-2	Sequence 2, Appl
29	361.5	11.6	855	4	US-09-664-600-2	Sequence 2, Appl
30	359.5	11.6	790	1	US-08-469-486-4	Sequence 54, Appl
31	359.5	11.6	790	2	US-08-469-468-4	Sequence 54, Appl
32	359.5	11.6	791	2	US-09-111-995-1	Sequence 1, Appl
33	359.5	11.6	791	2	US-08-832-0875-1	Sequence 1, Appl
34	359.5	11.6	791	3	US-08-112-145-4	Sequence 1, Appl
35	359.5	11.6	791	4	US-08-991-761A-6	Sequence 6, Appl
36	359.5	11.6	810	1	US-07-854-603-2	Sequence 2, Appl
37	359.5	11.6	810	1	US-08-147-000A-29	Sequence 29, Appl
38	359.5	11.6	810	3	US-09-086-514-1	Sequence 1, Appl
39	359.5	11.6	810	4	US-09-012-012-5	Sequence 5, Appl
40	359.5	11.6	810	6	5200340-8	Patent No. 5200340
41	358	11.5	454	3	US-09-518-046-2	Sequence 2, Appl
42	356.5	11.5	812	4	US-08-991-761A-7	Sequence 7, Appl
43	355.5	11.4	338	4	US-08-991-761A-10	Sequence 10, Appl
44	354.5	11.4	814	4	US-08-750-711-1	Sequence 1, Appl
45	354	11.4	407	4	US-09-734-675-4	Sequence 4, Appl

ALIGNMENTS

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RESULT 1
US-09-386-653A-7
; Sequence 7, Application US/09386653A
; Patent No. 6458564
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/09/386, 653A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-386-653A-7

Query Match          14.4%; Score 449; DB 4; Length 290;
Best Local Similarity 37.1%; Pred No. 2.4e-31;
Matches 89; Conservative 44; Mismatches 87; Indels 20; Gaps 6

QY      60  NTVGEGEPMQASVARGCAHICSGSLVADVTWLTAAHCEKAATELNSWSVLGSLQREG 119
DB      40  DTQGEPMQVYSIORNSHPFGSGLLIEQWLTAAHCHRNSTFSL--YQVILGARQLVQ 97

QY      120 LSPGAEEGVAAALQLPRAYNHYSQGSDLALLQLAHPTHT---PLCLQPAHRFPFGAS 175
DB      98  PGPFAWYARVRQVESNPFLQGTASSADVALVELAPVFTYIILPVCLPDPSPVIRETGMN 157

QY      176 CWATGW---DQDTSDAPGTLRNLRRLISRPCTNCIYNQ-----LHORHLSNPARPGML 226
DB      158  CWVWGWSPESEEDLLPEPRILQKLAAPVLIIDPPKCNLLYSKOTEFQYOPTIKN---DWL 213

QY      227 CGGQGPQVQGGCGGDSGGPVLCLEPDGHWQAGIISFASCAQEDAPVLLNTNTAHSWL 286
DB      214  CAGFEEGKDACKGDSSGPLVLVGGQ--WLQAGVISWEGCARQNRPGVYIRVTAAHHWVI 272

RESULT 2
US-09-387-375-7
; Sequence 7, Application US/09387375
; Patent No. 6485957
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Qi, Jensen

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1  TITLE OF INVENTION: DNA Encoding the Human Serine
2  TITLE OF INVENTION: Protease EOS
3  FILE REFERENCE: ORT-1031
4  CURRENT APPLICATION NUMBER: US/09/367,375
5  CURRENT FILING DATE: 1999-08-31
6  NUMBER OF SEQ ID NOS: 9
7  SOFTWARE: PatentIn Ver. 2.0
8  SEQ ID NO 7
9  LENGTH: 264
10 TYPE: PR1
11 ORGANISM: Homo sapiens
12 US-09-367-375-7

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Query Match 14.4%; Score 447; DB 31; length 284;
Best Local Similarity 40.7%; Pred. No. 3.5e-31;
Matches 101; Conservative 31; Mismatches 88; Gaps 7;

[illegible]

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1      RESULT 3
2      US-09-387-375-9
3      Sequence 9, Application US/09387375
4      Patent No. 6485957
5      GENERAL INFORMATION:
6      APPLICANT: Darrow, Andrew
7      APPLICANT: Andrade-Gordon, Patricia
8      APPLICANT: Qi, Jensen
9      TITLE OF INVENTION: DNA Encoding the Human Serine
10     TITLE OF INVENTION: Protease EOS
11     FILE REFERENCE: ORT-1031
12     CURRENT APPLICATION NUMBER: US/09/387,375
13     CURRENT FILING DATE: 1999-08-31
14     NUMBER OF SEQ ID NOS: 9
15     SOFTWARE: PatentIn Ver. 2.0
16     SEQ ID NO 9
17     LENGTH: 316
18     TYPE: PRT
19     ORGANISM: Artificial Sequence
20     FEATURE:
21     OTHER INFORMATION: Description of Artificial Sequence: Amino acid
22     OTHER INFORMATION: sequence of EOS tyrosinase fusion gene
23     US-09-387-375-9

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[illegible]

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QY 180 GMDQDTSAPGR-----LNRLRLLSRPTNCNIV-----QLHORHLSNAPRGM 226
Db 179 GWC---SLRPGVPLPEMRPLGVRPLPDSRTCGILYGVADVPQAEIRYL-----PGSL 230
QY 227 CGSPGPGVGPCCGSDSGFVLCEBPDGHWAOAGIISFASCAQEDAPVLLTNTAAHSSML 286
Dd 231 CAGYPGGHHKDACCGSDSGFPLTCLQ--SGSWLVGVVSWKGCALPNRPQVYTSVATYSPWI 289
QY 287 QAEVCGAA 294
Dd 290 QARVTSNA 297

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RESULT 4
US-09-386-653A-9
: Sequence 9, Application US/09386653A
: Patent No. 6458564
:
: GENERAL INFORMATION:
: APPLICANT: Andrade-Gordon, Patricia
: APPLICANT: Darrow, Andrew
: APPLICANT: Qi, Jian-shen
: TITLE OF INVENTION: DNA encoding the novel human serine
: TITLE OF INVENTION: protease T
: FILE REFERENCE: ORT-1032
:
: CURRENT APPLICATION NUMBER: US/09/386,653A
: CURRENT FILING DATE: 1999-08-31
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 9
:
: LENGTH: 315
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
: OTHER INFORMATION: of Protease T in a zymogen activation construct
US-09-386-653A-9

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	Query Match	14.4%;	Score 446;	DB 4;	Length 315;
	Best Local Similarity	37.3%;	Pred. No. 5e-31;		
	Matches	89;	Conservative 43;	Mismatches 85;	Indels 20; Gaps 6
QY	64	GEMPWQASVRRQACAI	CGSSLVADTWVLTAAHC	EKAATELNSKSVLGS	LQREGISPG 12
DB	61	GEMPWQVSIQRNMGSH	FCGSSLLAEQWVLTAAHC	CFNNTSETSL--	YQVLTGRQVLQSPGH 118
QY	124	AEEVGAALQLPRAVYHY	QSGSDLLALLOAHPHTT	----	PLCCPOPAAHRRPFASGCMAT 179
DB	119	AMAYARVOVESNPL	LYGTTASADVAVLVEAD	VPRTNITLVCLEPDS	VIFETGMNCWT 178
QY	180	GW-----DQTS	DAPGTLRLRLRLIS	RPTNCIYNQ-----	LHORHLSNPARPMGLGCP 230
DB	179	GWGSPSEBDLL	PERPRILQKLA	VPITIDTPKCNLLYS	KDTEFGYQPKTKN-----DMLCAGF 234
QY	231	QFVGQPCQGDSSG	GPLCLIEPDGHVVOAGIS	FASCAQEDAPVLLT	TAHSSWL 286
DB	235	EEBKQACKKDSG	GPLVLCVGQS--	WLQAGVLSWGGCA	RQNRPGVILRTVAHHNMI 289

RESULT 5
 US-08-944-483--66
 ; Sequence 66, Application US/08944483
 ; Patent No. 6232456
 ; GENERAL INFORMATION:
 ; APPLICANT: COHEN, MAURICE
 ; APPLICANT: COLPITTS, TRACEY L.
 ; APPLICANT: FRIEDMAN, PAULA N.
 ; APPLICANT: GRANADOS, EDWARD N.
 ; APPLICANT: KLASS, MICHAEL R.
 ; APPLICANT: RUSSELL, JOHN C.
 ; APPLICANT: STEWART, KENT D.
 ; APPLICANT: STROUPE, STEVEN D.
 ; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

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      TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
      NUMBER OF SEQUENCES: 76
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: Abbott Laboratories
      STREET: 100 Abbott Park Road
      CITY: Abbott Park
      STATE: IL
      COUNTRY: USA
      ZIP: 60064-3500
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Diskette
      OPERATING SYSTEM: DOS
      SOFTWARE: FASTSEQ for Windows Version 2.0
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/944,483
      FILING DATE:
      CLASSIFICATION: 424
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER:
      FILING DATE:
      ATTORNEY/AGENT INFORMATION:
      NAME: Becker, Cheryl L.
      REGISTRATION NUMBER: 35,441
      REFERENCE/DOCKET NUMBER: 6183.US.01
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 847/935-1729
      TELEFAX: 847/938-2623
      TELEX:
      INFORMATION FOR SEQ ID NO: 66:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 299 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: Linear
      US-08-944-483-66

Query Match          13.8%; Score 429.5; DB 3; Length 299;
Best Local Similarity 35.6%; Pred. No. 1,3e-29;
Matches 108; Conservative 47; Mismatches 103; Indels 45; Gaps 14;

QY      60 NTVPGEMPMQASVRROGAHICSGSLVDVTWLTAAHCFEKRAATELNSWSVLGSLQREG 119
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      6 SAVAGQMPQWQIVSYIEGVHVCGGSLVEQWVLSAHCFSPEHNKE--AYEVKLGAHQDS 63

QY      120 LSPCAEEVGVAALD--LPRAVNHYSQS--DLALLQLAHFTTHT---PLCLFPQPHRFP 171
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      64 YS---EDAKYSTLKDIIRHP-SYIOEGSOODIALQLSREITRSRYRIPICLPAANAASF 119

QY      172 FGASCMTATGWDDPTSD----APGLRLRLRLISRPCTNCITYQLQHRLSNPARPQMTC 227
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      120 NGLHCTYTGGHVAAPSLSLTPKLOOLEVPLISRETNCNLVINDAKPEEFHFVEDMVC 179

QY      228 GGPDPGVQPCQGSGSPVLCLBEDGHMVQAGIISFASSCAORDAPVLLTNIAASHSMIQ 287
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      180 AGYEKGSKDAQCGGSGGPLSC-PVEGLMYLTGIYSWDACGANRRPVYTLASTASYAMIQ 238

QY      288 ARV--QGAAPLAOSPETPENSDSCVACGS-----LR-----TAGPOAGAP 327
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      239 SKYTELEPRVV---POTQE-SQPDSTWL-CGSHLAFESAPAQGLIRPLFLPLGLALL 292

QY      328 SPW 330
       |||
Db      293 SPW 295

```

```

      APPLICANT: Darrow, Andrew
      APPLICANT: Qi, Jensen
      APPLICANT: Andrade-Gordon, Patricia
      TITLE OF INVENTION: Zymogen Activation System
      FILE REFERENCE: ORT-1028
      CURRENT APPLICATION NUMBER: US/09/386,642
      CURRENT FILING DATE: 1999-08-31
      NUMBER OF SEQ ID NOS: 60
      SOFTWARE: PatentIn Ver. 2.0
      SEQ ID NO 12
      LENGTH: 319
      TYPE: PRT
      ORGANISM: Artificial Sequence
      FEATURE:
      OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
      OTHER INFORMATION: with homo sapien serine protease catalytic domain
      US-09-386-642-12

Query Match      13.6%; Score 422; DB 4; Length 319;
Best Local Similarity 37.3%; Pred. No. 6,4e-29;
Matches 100; Conservative 46; Mismatches 94; Indels 28; Gaps 12

QY 64 GEMPWQASVRRQGHICSGSLVADTWLTAHCFEKAATELNSMSVVLGSLQREGSLSPG 123
Db 52 GQMPWQVSIYEGVHVCQGSILVSEQWLSAHCPSSEHNKE--AYEVKLGHHQDLSYS-- 107
QY 124 AEEVGVALQ--LPRAYNHSQGS--DLALQLAHPTTHT---PLCLPQPAHRRPFGAS 175
Db 108 -EDAKVSTLMDIIRHP-SYIQSGSGDIALQLQSRPIITFSYIRPICPAANASFPNGLH 165
QY 176 CWATGMDQDTSDD---APGTLRNLRRLISRPCTNCIYNQLHQHLSNPARPMICGSPQ 231
Db 166 CTVTGMSGHVAPSVSILTPKPLQQLLEVLISRETNCILYNIDAKDEEPRHFVQEDWVCAGYV 225
QY 232 PCVQGPCGDSGGGVLLLEPQGHVQAGIISFASSCAQEDBAPVLLTNTAAHSSWIAQV-- 290
Db 226 EGGKDAQCQSGSGGLSC-PVEGLWYLTGVISWGDACGARNPQGVYTLASYSASWISQKVT 284
QY 291 --QGAATLAQSPETPEMSDEDSVCACGS 316
Db 285 ELQPRVY----PQTQE-SQPPSNL-CGS 306

RESULT 7
US-09-386-642-11
; Sequence 11, Application US/09366642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
; US-09-386-642-11

Query Match      13.6%; Score 422; DB 4; Length 328;
Best Local Similarity 37.3%; Pred. No. 6,6e-29;
Matches 100; Conservative 46; Mismatches 94; Indels 28; Gaps 12

QY 64 GEMPWQASVRRQGHICSGSLVADTWLTAHCFEKAATELNSMSVVLGSLQREGSLSPG 123
Db 61 GQMPWQVSIYEGVHVCQGSILVSEQWLSAHCPSSEHNKE--AYEVKLGHHQDLSYS-- 116

```

```

QY 124 AEEVVAALQ--LPRAYNHYSOGS--DLALLQLAHPHTHT---PLCLPQPAHREFFGAS 175
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 117 -BDAXSTLKIDIIHPH-SYLOEGSQGDIALQLSRPITSRYIRPICLPAANAFENGJH 174
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 CWATGMDQDTSO----APCLTNLRRLRLSRPTCNCIYNQLOHRLHNSPARPGMLCGGPO 231
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 175 CTVTGWGHVAPSVSLTPRPLQOLEVPLISRETCLNYIDAKPEEPHVPQEDMCAGYV 234
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 PVOGFCQGDSDSGPVLCLEPPDGHVVOAGIISFASCAQEDAPVLLTNTAASSWLQARY- 290
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 235 EGGKACQGDSDSGGPLSC-PVEGLMYLTGIVSWGDCAGANRRGVYTLAASYSWIOSKYT 293
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 --QGAFLAQSPEPTPEMSDESDCVACGS 316
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 294 ELQPRVY---PQTOE-SQPDNL-CGS 315
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 8

US-09-386-629-7
Sequence 7, Application US/09386629
Patent No. 6426199

GENERAL INFORMATION:

APPLICANT: Darrow, Andrew L.

APPLICANT: Qi, Jensen

APPLICANT: Andrade-Gordon, Patricia

TITLE OF INVENTION: Identification and Characterization of the complementary

FILE REFERENCE: ORT-1030

CURRENT APPLICATION NUMBER: US/09/386,629

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 317

TYPE: PRT

ORGANISM: Homo sapiens

US-09-386-629-7

Query Match 12.9%; Score 400; DB 4; Length 317;

Best Local Similarity 30.8%; Pred. No. 5.3e-27;

Matches 99; Conservative 57; Mismatches 123; Indels 42; Gaps 11;

```

QY 27 CVCITTTVAIVNSLWMLSPFRKVOEPQ--GKAKRHGNTVPG-----EWPQASVROGAH 78
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 14 CIGTFSTLLASTALTNARIIPVPACGKPOQLNRVVGEDSTSEWPMIVISIQNGTH 73
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 79 ICGSGLVADTWVLTAAHCEKAAATELNS--WSVVLGSLQREGUSPGAEVVAALQLP 135
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 74 HCAGSLTISRWWITTAHCFK---DNLNRPYLFVSLGAWQLGNPGRSQKGVAMVE-P 128
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 136 RAYNHYSOG--SDALLQLAHPHTHT---PLCLPQPAHREFFGASCWATGW---DQDT 185
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 129 HHVYSWKEACADIALVRLERSIOFSERVLICLPASIHLPNTHCWISGMSIQDGVF 188
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 SDAPGTLRNRLRLSRPTCNCIYNQLOHRLHNSPARPGMLCGGPOPGVQFCQGDSDGP 245
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 189 LPHQTLQKLKVPITIDSEVCSHLV--WRGAGQGPITTEMLCAGYLEGRDCLDSDGP 245
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 246 VICLEPDGHVVOAGIISFASCAQEDAPVLLTNTAASSWLQARYVOGAFLAQSPEPTPM 305
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 246 LMC-QVDGAMLLAGIISWEGCAERNRPGVYISLSAHSRWEKIVQGVLRGAQ----- 299
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 306 SDESDCVACSLRTAGPQAGA 326
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 300 -----GGGALRAPSGSGA 313
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 9

US-09-386-629-8
Sequence 8, Application US/09386629
Patent No. 6426199

GENERAL INFORMATION:

```

| APPLICANT: Darrow, Andrew L.
| APPLICANT: Qi, Jensen
| APPLICANT: Andrade-Gordon, Patricia
| TITLE OF INVENTION: Identification and Characterization of the complementary
| FILE REFERENCE: ORT-1030
| CURRENT APPLICATION NUMBER: US/09/386,629
| CURRENT FILING DATE: 1999-08-31
| NUMBER OF SEQ ID NOS: 11
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 8
| LENGTH: 327
| TYPE: PRT
| ORGANISM: Artificial Sequence
| FEATURE:
| OTHER INFORMATION: Description of Artificial Sequence: C-E catalytic
| OTHER INFORMATION: domain fusion protein
| US-09-386-629-8

```

Query Match 12.5%; Score 388; DB 4; Length 327;

Best Local Similarity 32.7%; Pred. No. 6.2e-26;

Matches 90; Conservative 49; Mismatches 102; Indels 34; Gaps 9;

```

QY 65 EWPQASVROGAHICGSLVADTWVLTAAHCEKAAATELNS--WSVVLGSLQREGUS 121
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 62 EWPWIVSIOKNGTHHCAGSLTISRWWITTAHCFK---DNLNRPYLFVSLGAWQLGNPG 117
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 122 PGAEVVAALQLPRAAYNHYSOG--SDALLQLAHPHTHT---PLCLPQPAHREFFGAS 175
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 118 SRSQVGVAMVE-PHPVYSWKEACADIALVRLERSIOFSERVLICLPDASIHLPNTH 176
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 CWATGW---DQDTSAPGTLRNRLRLSRPTCNCIYNQLOHRLHNSPARPGMLCGGPO 231
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 177 CWISGMSIQDGVPLPHQTLQKLKVPITIDSEVCSHLV--WRGAGQGPITTEMLCAGYL 233
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 PVOGFCQGDSDSGPVLCLEPPDGHVVOAGIISFASCAQEDAPVLLTNTAASSWLQARY 291
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 234 EGERDACLGDSDSGPLMC-QVDGAMLLAGIISWEGCAERNRPGVYISLSAHSRWEKIVQ 292
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 292 GAAFLAQSPEPTPEMSDESDCVACSLRTAGPQAGA 326
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 293 GVLRRGAQ-----GGGALRAPSGSGA 315
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 10

US-09-644-600-10
Sequence 10, Application US/09644600
Patent No. 6451500

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Tanimoto, Hirotooshi

TITLE OF INVENTION: Overexpressed in Carcinomas

FILE REFERENCE: D6064CIP/D

CURRENT APPLICATION NUMBER: US/09/644,600

CURRENT FILING DATE: 2000-08-23

PRIOR APPLICATION NUMBER: 09/421,213

PRIOR FILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: 09/027,337

PRIOR FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 10

LENGTH: 902

TYPE: PRT

ORGANISM: Mus musculus

FEATURE:

OTHER INFORMATION: Epithin

US-09-644-600-10

Query Match 12.1%; Score 375; DB 4; Length 902;

Best Local Similarity 33.3%; Pred. No. 3.4e-24;

Matches 92; Conservative 38; Mismatches 114; Indels 32; Gaps 9;

QY 44 SPRKVOEPOGKAKRHGNTVPGEMWQASVRRQG-AHICSGSLVADTWLTAHCFE---K 99
DB 608 SFTK---QARVGGTINADDEGEMWQVSIHALGQCHLGCASLISPDWLVSAAHCFQDDKN 663
QY 100 AATELNWSVVLGSLQREGLSPGAEEVVALQJLPR-----AYNHVSQSGDLALQL- 152
DB 664 FKYSYTWMTATLGLLDDSKRSAS---CVCGLKLRITTHSPFDDFTDYIALLELEK 719
QY 153 --AHPTHTPLCLPPAHRFPGASCWATGMDODTSDAGT--LRLRLRLISRPCTNCI 208
DB 720 SVEYSTVVRPILCPATHVFPAKAIWGTGHTKEGTGALILQKEIRIVINQTTCEDL 779
QY 209 YNQLHQRHLSNARPGMLCGSPQVQPCQDSDGSPVLCLEPDDHWNQAGIISFASSGA 268
DB 780 MPQ-----QITPRMNCVGFSLGSDVSCQDGPLSSABEKDRMFGAGVAVSWGEGCA 831
QY 269 QEDAPVLLTNTAAHSSWMLQARVQG-AAFLAQSPETP 303
DB 832 QRNKRGVYTRLPCCSSGLDORAHWGIAAWTDSRPQTP 867

RESULT 11

US-08-991-761A-13
Sequence 13, Application US/08991761A
Patent No. 6576609
GENERAL INFORMATION:
APPLICANT: Soft, Gerald
APPLICANT: Gately, Stephen
APPLICANT: Twardowski, Przemyslaw
TITLE OF INVENTION: "Methods and Compositions for Generating
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,761A
FILING DATE:
CLASSIFICATION: 1642
ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wanneil M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3501-16-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-991-761A-13

Query Match

Best Local Similarity 11.9%; Score 370.5; DB 4; Length 790;
Matches 90; Conservative 49; Mismatches 101; Indels 39; Gaps 12;

QY 23 LVDPCIVC--CITTYAIVNSLWMLSF---RKVOEPOGKAKRHQN--TVPGEMWQASVR- 73
DB 531 LRDYCVVPCVVS-----SFDGKRPKEPKCPARVVGGCVSISHSNPMQISLRY 580
QY 74 RQGAHICGSLVADTWLTAHCFEKAATELNSWSVVLGSLQREGLSPGAEEVVALQ 133

DB 561 RYRHFCCGTLISPEWVLTAAHCLIEKSSP--SSYKVLGAHEEYHLEGEQVIDSVKLI- 637
QY 134 LPRAYNHVSQSDLLALQLAHPTHT---PLCLPPAHRRPFGASCWATGMDODTSD-A 188
DB 638 ---FKERSE-ADIALTLSSPAVITDKVIPACLPYVAVADRACVITTMGETKGYTG 692
QY 189 PGLRLNLRLISRPCTNCIYNQLHQRHLSNARPGMLCGSPQVQPCQDSDGSPVLC 248
DB 693 AGLLKEARLPVIENTKCN-----RYEVLGKRVSENEICAGHLAGGIDSCQDSSGSPVLC 746
QY 249 LEPDGHWQAGIISPASSCAQEDAPVLLTNTAAHSSWMLQ 287
DB 747 FEKDKYILQ-GVTSWGLGALPNKRGVYVRSRYTWIE 784

RESULT 12

US-08-248-629A-1
Sequence 1, Application US/08248629A
Patent No. 5639725
GENERAL INFORMATION:
APPLICANT: Folkman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: "Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: Macintosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,629A
FILING DATE: 04/26/94
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Larry W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 812
TYPE: amino acid
TOPOLOGY: linear
US-08-248-629A-1

Query Match

Best Local Similarity 11.9%; Score 369.5; DB 1; Length 812;
Matches 93; Conservative 45; Mismatches 107; Indels 39; Gaps 11;

QY 23 LVDPCIVCITTYAIVNSLWMLSFVRKVOEPOGKAKR-HGNTV-----PGEMWQASVRRQ 75
DB 551 LRDYCDIPICASA-----SFECKGRQVEPKCPGRVGGCVANPSWPMQISLRTK 602
QY 76 --GAHICGSLVADTWLTAHCFEKAATELNSWSVVLGSLQREGLSPGAEEVVALQ 133
DB 603 FPGGPFCCGTLAPRWVLTAAHCLIEKSSRPER--YKVLGAHEBYIRGLDVEISVAKLI 660
QY 134 LPRAYNHVSQSDLLALQLAHPTHT---PLCLPPAHRRPFGASCWATG--DQDTS 187
DB 661 LE-----PNNRDIALKLISRPATITDVIPACLPSPYVAVADRITCYITGGETGTFG 714


```

RESULT 15
US-08-326-785-1
; Sequence 1, Application US/08326785
; Patent No. 5792845
; GENERAL INFORMATION:
; APPLICANT: Folkman, Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Angiostatin and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/326,785
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,629
; FILING DATE: 04/26/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Larry W. Stults, Ph.D.
; REGISTRATION NUMBER: 34,025
; REFERENCE/DOCKET NUMBER: 05213-0121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 812
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-326-785-1
Query Match 11.9%; Score 369.5; DB 1; Length 812;
Best Local Similarity 32.7%; Pred. No. 9e-24;
Matches 93; Conservative 45; Mismatches 107; Indels 39; Gaps 11;

QY 23 LYDFCIVCITTYAINVLSMLMLSFVKVOEPQSKAR-HGNTV-----PGEWPMQASVRRQ 75
Db 551 LYDVCIDPILCASAE-----SFECKGRPYEPKPCPRVAVGGCVANPHSWPMQISLTR 602
QY 76 --GAGICGSLVADPTWVLTAAHCPEKAATELNSKSVTLGSLQEBGSLPAGAEVGVAAIQ 133
Db 603 FTGGHFCGCGTLIAEPWVLTAAHCLEKSSRPFF--YKVLGAHEEYIRGLDVEISVAKLI 660
QY 134 LPRAVNHYSQGSDDLALQLAHPHTHT-----PLCLPOPAPHRPPFGASCWATGM--DOPSTD 187
Db 661 LE-----PNNRDIALALKLSRPATITTDKVIYACLPSPRYMWADRTICITWGEGTGTGFG 714
QY 188 APGTLRNLRLLRISRPNTCINYQLHQHRLSNPARPGMLCGGPGOPGVGPCQSGSGGPGVL 247
Db 715 A-GRLEKEQLVIEIKVENCVR-----EYLNRRVXSTELCAGOLAGGVDSQCGDSGGGPLY 767
QY 248 CLEPDGHVVOAGIISFASSCAOEDAPVLLTNTTAHSSWLGARVQ 291
Db 768 CPEKDKYILQ--GVTSWGLGCAKPNKPGVYVRSRFDVIEEEM 810

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Search completed: January 6, 2004, 10:03:44
Job time : 22 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2004, 09:55:11 ; Search time 47 Seconds
(without alignments)
1928.359 Million cell updates/sec

Title: US-09-978-194A-132

Perfect score: 3108
Sequence: 1 MLSSLVSLAGSVIAMIIF.....PEPEAPGSCANISQPTSC 571

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A.Geneseq.19Jun03.*
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
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9: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
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16: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
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19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	3108	100.0	571	20 AAY41704
2	3108	100.0	571	21 AAB44260
3	3108	100.0	571	21 AAB24096
4	3108	100.0	571	24 AAB61090
5	2809.5	90.4	628	23 AAU82728
6	2809.5	90.4	628	24 AAB72375
7	2779.5	89.4	642	24 AAB72374
8	2304	74.1	552	23 AAB21440
9	1454	46.8	267	21 AAY90291

10	1436	46.2	267	22 AAB20156	Human protein SECP
11	1346	43.3	267	24 AAB72373	Transmembrane seri
12	1023	32.9	198	22 AAB20162	Human protein SECP
13	1003.5	32.3	219	21 AAY72095	Human serine prote
14	896.5	28.8	301	22 AAG67515	Amino acid sequenc
15	885	28.5	255	22 AAG67514	Amino acid sequenc
16	793	25.5	818	23 ABB98135	Human PKM Incyte
17	793	25.5	818	23 AAU82753	Amino acid sequenc
18	724	23.3	766	22 AAM93568	Human polypeptide,
19	665.5	21.4	691	23 AAE14348	Human protease PRT
20	636.5	20.5	1128	23 AAU98890	Human protease PRT
21	636.5	20.5	1128	23 AAU82739	Amino acid sequenc
22	557.5	17.9	357	23 ABB09524	Human prostaticin pr
23	556	17.9	344	23 ABB09523	Human prostaticin pr
24	490	15.8	986	24 ABBU12065	Human NOVI2a CG922
25	476.5	15.3	1031	23 ABB60993	Novel human protei
26	450	14.5	328	22 AAM41174	Human polypeptide
27	449	14.4	272	23 ABB07286	Human protease T.
28	449	14.4	290	21 AAY73388	Human protease T.
29	449	14.4	290	22 AAU12282	Human gene 4 encod
30	449	14.4	290	22 AAE03821	Human albumin fusi
31	449	14.4	290	22 AAB73945	Human albumin fusi
32	449	14.4	290	23 ABB66545	Human PRO polypept
33	449	14.4	290	24 ABB66680	Human serine prote
34	449	14.4	290	24 ABB66956	Human secreted/cra
35	449	14.4	290	24 ABBG73394	Novel secreted and
36	449	14.4	290	24 ABBU59761	Amino acid sequenc
37	449	14.4	297	19 AAM77304	Primate LP294. Ma
38	448	14.4	280	23 ABBG91414	Novel human protei
39	448	14.4	280	23 ABB61010	Novel human protei
40	448	14.4	282	23 ABB61011	Tissue plasminogen
41	447.5	14.4	794	10 AAB90179	Human serine prote
42	447	14.4	284	22 AAU00467	Recombinant human
43	447	14.4	316	22 AAU00468	Fusion protein of
44	446	14.4	315	22 AAB73946	Human prostaticin-I
45	445	14.3	262	23 ABB07284	

ALIGNMENTS

RESULT 1	AAV41704	standard; Protein; 571 AA.
ID	AAV41704;	
XX	AAV41704;	
AC	AAV41704;	
XX	07-DEC-1999	(first entry)
DT	07-DEC-1999	
XX	Human PRO351	protein sequence.
DE	Human PRO351	protein sequence.
XX	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;	
KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder;	
KW	secreted protein; transmembrane protein.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WO9946281-A2.	
PN	WO9946281-A2.	
XX	16-SEP-1999.	
PD	16-SEP-1999.	
XX	08-MAR-1999;	99WO-US05028.
PF	08-MAR-1999;	99WO-US05028.
XX	10-MAR-1998;	98US-0077450.
PR	11-MAR-1998;	98US-0077632.
PR	11-MAR-1998;	98US-0077641.
PR	11-MAR-1998;	98US-0077649.
PR	12-MAR-1998;	98US-0077791.
PR	13-MAR-1998;	98US-0078004.
PR	17-MAR-1998;	98US-0040220.
PR	20-MAR-1998;	98US-0078886.
PR	20-MAR-1998;	98US-0078910.
PR	20-MAR-1998;	98US-0078936.

PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 23-APR-1998; 98US-0083335.
PR 27-APR-1998; 98US-0083322.
PR 28-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083559.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.

PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
PA (GETH) GENENTECH INC.
XX
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
PI
XX
XX WPI; 1999-551358/46.
DR N-PSDB; AA234002.
XX
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
XX
PS Claim 12; Fig 49; 530pp; English.
XX
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA233891 to
CC AA234338, and AA41685 to AA41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
XX
SQ Sequence 571 AA;

Query Match 100.0%; Score 3108; DB 20; Length 571;
Best Local Similarity 100.0%; Pred. No. 2,5e-207;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSSLSVSLAGSVLWMLFVLYDFCICTTVAINVSLMWLSFRKVOEPGKAKRRGN 60
DB 1 MLSSLSVSLAGSVLWMLFVLYDFCICTTVAINVSLMWLSFRKVOEPGKAKRRGN 60

QY 61 TVPGEMPQASVRRGGAHICGSLVADTWVLTAAACFEKAAATELNSVVGSLQREG 120
DB 61 TVPGEMPQASVRRGGAHICGSLVADTWVLTAAACFEKAAATELNSVVGSLQREG 120

QY 121 SPGAEVGVAAALQLPRAVNHYSQGSDDLQLAHFTTTPCLCPARFRPGASCWATG 180
DB 121 SPGAEVGVAAALQLPRAVNHYSQGSDDLQLAHFTTTPCLCPARFRPGASCWATG 180

QY 181 WDQDTSAPGTLRLNRLRLISPTCNCIYNQHQHRLSNPARPGMLCGPGQVGPCCG 240
DB 181 WDQDTSAPGTLRLNRLRLISPTCNCIYNQHQHRLSNPARPGMLCGPGQVGPCCG 240

QY 241 DSGGPVLCLEPDGHVVOAGIISFASSCAQEDAPVLLTTAAHSSVLQARVQGAALQASP 300
DB 241 DSGGPVLCLEPDGHVVOAGIISFASSCAQEDAPVLLTTAAHSSVLQARVQGAALQASP 300

QY 241 DSGGPVLCLEPDGHVVOAGIISFASSCAQEDAPVLLTTAAHSSVLQARVQGAALQASP 300
DB 241 DSGGPVLCLEPDGHVVOAGIISFASSCAQEDAPVLLTTAAHSSVLQARVQGAALQASP 300

QY 301 ETPMSDEDSVCVACSLRTAGPQAGAPSPWPEARLHMGOGLACGALVSEAVLTTAAHC 360
DB 301 ETPMSDEDSVCVACSLRTAGPQAGAPSPWPEARLHMGOGLACGALVSEAVLTTAAHC 360

QY 361 FIGRAPEEWSVGLTRPEEWGLKQLIHGAYTHREGVDALLLAAQVTLGASLRPLC 420
DB 361 FIGRAPEEWSVGLTRPEEWGLKQLIHGAYTHREGVDALLLAAQVTLGASLRPLC 420

QY 421 LPYPDHHLPDGERGVNLGRAPGAGISSLQTVPVTLCPACRSRLHAAPGDSPIPLGM 480
DB 421 LPYPDHHLPDGERGVNLGRAPGAGISSLQTVPVTLCPACRSRLHAAPGDSPIPLGM 480

QY 481 VCTSAVGLPSCGEGISGAPLVHEVNGTWFLAGHSFGACCGAPAPAYFTALPAEDVWS 540
DB 481 VCTSAVGLPSCGEGISGAPLVHEVNGTWFLAGHSFGACCGAPAPAYFTALPAEDVWS 540

QY 541 SLDWVFAEPEPEAERPGSCLANISOPTSC 571
 DB 541 SLDWVFAEPEPEAERPGSCLANISOPTSC 571
 RESULT 2
 AAB44260
 ID AAB44260 standard; Protein; 571 AA.
 XX AAB44260;
 AC
 XX 08-FEB-2001 (first entry)
 DT
 XX Human PRO351 (UNQ308) protein sequence SEQ ID NO:132.
 DE
 XX Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
 KW expressed sequence tag; detection; cancer.
 XX Homo sapiens.
 OS
 PN WO200053756-A2.
 XX 14-SEP-2000.
 PD
 XX 18-FEB-2000; 2000WO-US04341.
 PF
 XX 08-MAR-1999; 99WO-US05028.
 XX 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Klishvin IJ, Kuo SS, Napier MA, Pan J, Pooni NF, Roy MA,
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
 XX
 XX WPI: 2000-611443/58.
 DR N-PSDB; AAC78486.
 DR
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 XX
 PS Claim 12; Fig 49; 636pp; English.
 XX
 XX AAC78486 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.

XX SQ Sequence 571 AA;
 Query Match 100.0%; Score 3108; DB 21; Length 571;
 Best Local Similarity 100.0%; Pred. No. 2,5e-207;
 Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSSLSVSLAGSVYLAHLPFLVDFPCITTTVAIVNSLWLSFRKVOEPQAKRRGN 60
 DB 1 MLSSLSVSLAGSVYLAHLPFLVDFPCITTTVAIVNSLWLSFRKVOEPQAKRRGN 60
 QY 61 TVPGEMWQASVRRQGAHICGSLVADPTWVLTAAHCEKAATLNSVSLGSLQREG 120
 DB 61 TVPGEMWQASVRRQGAHICGSLVADPTWVLTAAHCEKAATLNSVSLGSLQREG 120
 QY 121 SPGAEEVVALQIPRAYNHYSQGSDDLALQLAHPTHTPLCLPQPAHFPFGASCWATG 180
 DB 121 SPGAEEVVALQIPRAYNHYSQGSDDLALQLAHPTHTPLCLPQPAHFPFGASCWATG 180
 QY 181 WDQDTSAPGTLRLRLISRPTCNCTYNQHQHLSNPARPGMLCGGPQGVQPCQG 240
 DB 181 WDQDTSAPGTLRLRLISRPTCNCTYNQHQHLSNPARPGMLCGGPQGVQPCQG 240
 QY 241 DSGGPVLCLEPDGHWVQAGIISFASSCQEDAPVLTNTAAHSSWLQARVQGAFLAOSP 300
 DB 241 DSGGPVLCLEPDGHWVQAGIISFASSCQEDAPVLTNTAAHSSWLQARVQGAFLAOSP 300
 QY 301 ETPEMSDSCVACGSILRTAGPQAGSPWPMERLHMQGLACGALVSEAVLTAAHC 360
 DB 301 ETPEMSDSCVACGSILRTAGPQAGSPWPMERLHMQGLACGALVSEAVLTAAHC 360
 QY 361 FIGRAPEPEWSVGLGTRPEEWGLKQLIHGAYTTPREGGYDMLLALQPVTLGASLRPLC 420
 DB 361 FIGRAPEPEWSVGLGTRPEEWGLKQLIHGAYTTPREGGYDMLLALQPVTLGASLRPLC 420
 QY 421 LPYPDHLPDGERGWLGRARPGAGISGLQTVPTLLCPKRCSLHAAFGDGSFILPGM 480
 DB 421 LPYPDHLPDGERGWLGRARPGAGISGLQTVPTLLCPKRCSLHAAFGDGSFILPGM 480
 QY 481 VCTSAVGEPLSCGEGLSGAPLVHEVRGTWFLAGHSFGDAGCGPARPAFTALPAVEDWS 540
 DB 481 VCTSAVGEPLSCGEGLSGAPLVHEVRGTWFLAGHSFGDAGCGPARPAFTALPAVEDWS 540
 QY 541 SLDWVFAEPEPEAERPGSCLANISOPTSC 571
 DB 541 SLDWVFAEPEPEAERPGSCLANISOPTSC 571
 RESULT 3
 AAB24046
 ID AAB24046 standard; Protein; 571 AA.
 XX AAB24046;
 AC
 XX 25-JAN-2001 (first entry)
 DT
 XX
 DE Human PRO351 protein sequence SEQ ID NO:12.
 XX
 XX Human; tumour; diagnosis; neoplastic disease; identification; cancer;
 KW tumorigenesis; detection; neoplastic cell growth; proliferation;
 KW cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
 KW immunological disorder.
 XX
 OS Homo sapiens.
 PN WO200053754-A1.
 XX 14-SEP-2000.
 PD
 XX 06-JAN-2000; 2000WO-US00277.
 PF
 XX 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.

22-MAR-2001; 2001WO-US09552.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 11-MAR-1998; 98US-077649P.
PR 12-MAR-1998; 98US-077791P.
PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-078939P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 27-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 30-MAR-1998; 98US-079923P.
PR 26-MAY-1998; 98US-0267213.
PR 17-MAR-1998; 98US-0040220.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 02-NOV-1998; 98US-0184216.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 22-DEC-1998; 98US-0218517.
PR 05-MAR-1999; 99US-0254465.
PR 10-MAR-1999; 99US-0265686.
PR 12-APR-1999; 99US-0284291.
PR 14-MAY-1999; 99US-0311832.
PR 14-MAY-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380142.
PR 08-NOV-2000; 2000US-0709238.
PR 27-NOV-2000; 2000US-0723749.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 22-MAR-2001; 2001US-0816920.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Baker KP, Botstein D, Deanoys L, Eaton D;
PI Ferrara N, Flivarooff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Kildavard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kildavin IU, Kuo SS, Napier MA, Pan J, Paoletti NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI: 2003-288163/28.
DR N-PSDB; ABX92374.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies
XX
XX Claim 12; Fig 49; 459p; English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists. The
CC bioactive molecule may be a toxin, radiolabel or antibody, and causes
CC apoptosis or death of the cell. The PRO polypeptides are useful for
CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
CC cardiac insufficiency, nervous system disorders, kidney disorders,
CC bone and cartilage disorders or arthritis, tumours, and wound healing.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, for the genetic
CC analysis of individuals with genetic disorders, and in gene therapy.
CC ABU61071-ABU61164 represent the human PRO polypeptides of the
CC invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdidentry.html.
XX
SQ Sequence 571 AA;
Query Match 100.0%; Score 3108; DB 24; Length 571;
Best Local Similarity 100.0%; Pred. No. 2,56-207;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLSSLSVSLAGSVLIAMILFVLVDYFCIVCTTYAINVSLMWLSFRKYOEPOGKAKRHGN 60
DB 1 MLSSLSVSLAGSVLIAMILFVLVDYFCIVCTTYAINVSLMWLSFRKYOEPOGKAKRHGN 60
QY 61 TTPGEMPWQASVVRQGAHICSGSLVADPTWVLTAAACEKKAATEINSSVVGSIQREGL 120
DB 61 TTPGEMPWQASVVRQGAHICSGSLVADPTWVLTAAACEKKAATEINSSVVGSIQREGL 120
QY 121 SPGAEEVVAALQLPRAVNHYSQSGDLALQLAHTTTPPLCLPPARFPFGASCWATG 180
DB 121 SPGAEEVVAALQLPRAVNHYSQSGDLALQLAHTTTPPLCLPPARFPFGASCWATG 180
QY 181 WDQTSAPGTLRLRLRLISRPCTNCIYNQLHQRHLSNPARPGMLCGGPQPGVGCQCG 240
DB 181 WDQTSAPGTLRLRLRLISRPCTNCIYNQLHQRHLSNPARPGMLCGGPQPGVGCQCG 240
QY 241 DSGGPVLCLEPDGHVQAGIISFASSCQOEDAPVLLTNTAAHSSVLOARVQGAFLAOSP 300
DB 241 DSGGPVLCLEPDGHVQAGIISFASSCQOEDAPVLLTNTAAHSSVLOARVQGAFLAOSP 300
QY 301 ETPEMSDSDSCVACGSLTAGPQAGAPSPWPEARLHMQGLACGALVSEAVLTTAHC 360
DB 301 ETPEMSDSDSCVACGSLTAGPQAGAPSPWPEARLHMQGLACGALVSEAVLTTAHC 360
QY 361 FIGRQAPPEWSVGLCTREEWGLKQLIHGAYTHREGGYDMALLLAAQPVTLGASLRPLC 420
DB 361 FIGRQAPPEWSVGLCTREEWGLKQLIHGAYTHREGGYDMALLLAAQPVTLGASLRPLC 420
QY 421 LPYPDHHLPDGERGVNLGRARPAGISSLQTVPTVTLCPRACSRLLHAAPGGDPSITLPM 480
DB 421 LPYPDHHLPDGERGVNLGRARPAGISSLQTVPTVTLCPRACSRLLHAAPGGDPSITLPM 480
QY 481 VQTSVAGLPSCEGSGAPLVHEVGTWFLGHSFGACGCPARPAFTALPAYEDWVS 540
DB 481 VQTSVAGLPSCEGSGAPLVHEVGTWFLGHSFGACGCPARPAFTALPAYEDWVS 540
QY 541 SLDMQVYFAEBEPPEABPQSCLANISQPTSC 571
DB 541 SLDMQVYFAEBEPPEABPQSCLANISQPTSC 571
RESULT 5
AAU82728

ID AAU82728 standard; Protein, 628 AA.
 AC AAU82728;
 XX
 XX
 DT 23-APR-2002 (first entry)
 DE Amino acid sequence of novel human protease #27.
 XX
 XX Human; protease; cancer; immune-related disorder; cardiovascular disease;
 KW neuronal-associated disease; metabolic disorder; inflammatory disorder;
 KW nervous system disorder; sexual dysfunction; pain; mood disorder;
 KW hypertension; psychotic disorder; neurological disorder; dyskinesia;
 KW viral infection; human immunodeficiency virus; HIV; non-viral infection;
 XX ocular disease; cytoskeletal; enzyme.
 XX
 OS Homo sapiens.
 PN WO200200860-A2.
 XX
 XX 03-JAN-2002.
 PD
 XX 26-JUN-2001; 2001WO-US20171.
 PF
 XX 26-JUN-2000; 2000US-214047P.
 PR
 XX (SUGB-) SUGEN INC.
 PA
 PI Plowman G, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
 PI Charyczak G;
 XX
 DR WPI; 2002-139913/18.
 DR N-PSDB; ABK31770.
 XX
 PT Nucleic acids encoding novel human proteases, useful for useful for
 PT treating diseases and disorders such as cancers, immune-related
 PT diseases and disorders, cardiovascular disease (e.g. stenosis) and
 PT inflammatory disorders.
 DE
 PS Claim 6; Fig 2K; 313pp; English.
 XX
 XX The present invention relates to the isolation of novel human
 CC proteases, and the nucleic acids encoding them. The sequences of
 CC the invention are useful for treating diseases and disorders such as
 CC cancers (e.g. breast, colon, lung), immune-related diseases and disorders
 CC (e.g. inflammatory diseases and asthma), cardiovascular diseases
 CC (e.g. stenosis and coronary thrombosis), brain or neuronal-associated
 CC diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory
 CC disorders (e.g. rheumatoid arthritis and psoriasis), central or
 CC peripheral nervous system diseases, migraines, pain, sexual dysfunction,
 CC mood disorders, attention disorders, cognition disorders, hypotension,
 CC hypertension, psychotic disorders, neurological disorders
 CC (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias.
 CC The nucleic acids and polypeptides are also useful for treating viral
 CC infections caused by human immunodeficiency virus (HIV), and non-viral
 CC infections such as ocular disease (e.g. glaucoma) and macular
 CC degeneration. AAU82702-AAU82760 represent the novel human proteases of
 CC the invention.
 CC
 SQ Sequence 628 AA;
 QY Query Match 90.4%; Score 2809.5; DB 23; Length 628;
 DB Best Local Similarity 98.5%; Pred. No. 1,4e-186;
 DB Matches 516; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
 QY 49 QEPQCAK-RHGVTVGEMPMQASVVRQGAHITSGSLVADTWLTLAHCPEKAAATELNS 107
 DB 105 QGPGPPKQEGNTVGEPMWQASVVRQGAHITSGSLVADTWLTLAHCPEKAAATELNS 164
 QY 108 MSVVLGSLREGHSPAAEEVGAVALQPPRVNHYSGSDPLALLQHPHTTPTLCPOPA 167
 DB 165 MSVVLGSLREGHSPAAEEVGAVALQPPRVNHYSGSDPLALLQHPHTTPTLCPOPA 224
 QY 168 HRFPGASCWATGMDTSDAPGTLNRLRLISPTNCIYNQLHQRHLSPARPGLMC 227

DB 225 HRFPGASCWATGMDTSDAPGTLNRLRLISPTNCIYNQLHQRHLSPARPGLMC 284
 QY 228 GGPQGVGPGCOGDSGSPVLCLEPDGHVQAGIIFSSACQAEADPVLITNTAAHSMWQ 287
 DB 285 GGPQGVGPGCOGDSGSPVLCLEPDGHVQAGIIFSSACQAEADPVLITNTAAHSMWQ 344
 QY 288 ARVGAFLAQSPTPEMSDESDSCVACSLRTAGQAGAPSPFWPEARLIMOGQLACGA 347
 DB 345 ARVGAFLAQSPTPEMSDESDSCVACSLRTAGQAGAPSPFWPEARLIMOGQLACGA 404
 QY 348 LVSEAVLITAAHCFIQRQAPPEMSVGLSTREPMWLKQLIHGATTHREGVDMALLLA 407
 DB 405 LVSEAVLITAAHCFIQRQAPPEMSVGLSTREPMWLKQLIHGATTHREGVDMALLLA 464
 QY 408 QPVTGASLRPLCLPYPPHLLPDGGRGWLGRAPGAGISSLOTVPVLLGPACSRLLHA 467
 DB 465 QPVTGASLRPLCLPYPPHLLPDGGRGWLGRAPGAGISSLOTVPVLLGPACSRLLHA 524
 QY 468 AFGDGSFILPGMWTSAVGBLPSCEGLSGAPLVHEVGTWFLAGLSFGDACQGPAPPA 527
 DB 525 AFGDGSFILPGMWTSAVGBLPSCEGLSGAPLVHEVGTWFLAGLSFGDACQGPAPPA 584
 QY 528 VFTALPAYEDWVSLDMQVYFAEPEPEAPRSCIANISQPTSC 571
 DB 585 VFTALPAYEDWVSLDMQVYFAEPEPEAPRSCIANISQPTSC 628
 RESULT 6
 ABP72375
 ID ABP72375 standard; Protein, 628 AA.
 XX
 AC ABP72375;
 XX
 DT 13-MAY-2003 (first entry)
 XX
 DE Transmembrane serine protease 20 (MTSP20) polypeptide.
 XX
 KW Human; transmembrane serine protease 20; MTSP20; enzyme;
 KW endothelase; cytoskeletal; dermatological; cardiac; vulnerary;
 KW ophthalmological; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003004681-A2.
 PD
 PD 16-JAN-2003.
 PF 03-JUL-2002; 2002WO-US21208.
 PR 03-JUL-2001; 2001US-302339P.
 PA (CORV-) CORVAS INT INC.
 PI Madison EL, Ong EO;
 PI WPI; 2003-239207/23.
 DR
 XX
 PT New type-II membrane-type serine protease 20 polypeptides, useful for
 PT preparing a medicament for diagnosing, treating or preventing cancer,
 PT dermatological disorders, aberrant wound repairs or crest syndromes -
 PS Claim 42; Page 213-215; 216pp; English.
 XX
 CC The present sequence is the protein sequence of novel human type
 CC II transmembrane serine protease 20 (MTSP20), an endothelial cell
 CC transmembrane protein (endothelase) that is expressed in oesophageal,
 CC tumour tissues, in lung carcinoma, colon, cervix, leukaemia and other
 CC cell lines as well as in certain healthy cells and tissues. The
 CC level of MTSP20 can be diagnostic of prostate, uterine, lung,
 CC oesophagus or colon cancer, or leukaemia. The expression and/or
 CC activation of MTSP20 on, or in the vicinity of, a cell or a
 CC bodily fluid can be a marker for breast, prostate, lung, colon and

other cancers. The invention provides MTSP20 polypeptides and protease domains, zymogen and activated forms, single and multi chain forms, the nucleic acids encoding them, probes and primers, expression vectors, host cells, antibodies and transgenic animals. Nucleic acids encoding MTSP20 or its protease domain can be expressed in a host cell, and the protein used in assays to identify candidate compounds that modulate MTSP activity. A claimed method of inhibiting tumour initiation, growth or progression or for treating a malignant or pre-malignant condition, especially of the breast, cervix, prostate, lung, ovary or colon, involves administering an inhibitor of a MTSP20 polypeptide, especially an antisense oligonucleotide, double-stranded RNA or antibody (all claimed). These inhibitors are also used in a claimed method of treating or preventing a disease or disorder associated with undesired and/or uncontrolled angiogenesis or neovascularisation, especially undesired angiogenesis associated with solid neoplasms, vascular malformations and cardiovascular disorders (especially angiofibroma, angiolipoma, atherosclerosis, restenosis/refluxion injury, arteriovenous malformations, haemangiomas and vascular adhesion, dyschondroplasia with vascular hamartoma (Fafucci's syndrome), hereditary haemorrhagic telangiectasia (Rendu-Osler-Weber syndrome) and von Hippel Lindau syndrome), chronic inflammatory diseases (especially diabetes mellitus, haemophilic joints, inflammatory bowel disease, nonhealing fractures, periodontitis, psoriasis, rheumatoid arthritis, venous stasis ulcers, granulations-burns, hypertrophic scars, liver cirrhosis, osteoradionecrosis, postoperative adhesions, pyogenic granuloma and systemic sclerosis), aberrant wound repairs, circulatory disorders (especially Raynaud's phenomenon), crest syndromes (especially calcinosis, oesophageal, dyonotolcy, sclerodactyly and telangiectasis), dermatological disorders (especially systemic vasculitis, scleroderma, pyoderma gangrenosum, vasculopathy, venous, arterial ulcers, Sturge-Weber syndrome, Post-wine stains, blue rubber, bleb naevus syndrome), Klippel-Trenaunay-Weber syndrome and Osler-Weber-Rendu syndrome) and ocular disorders (especially blindness caused by ocular neovascular disease, corneal graft neovascularisation, macular degeneration in the eye, neovascular glaucoma, trachoma, diabetic retinopathy, myopic degeneration, retinopathy of prematurity, retrolental fibroplasia and corneal neovascularisation).

Query Match	90.4%	Score 2809.5	DB 24	Length 628
Best Local Similarity	98.5%	Pred. No. 1.4e-186		
Matches 516	Conservative 1	Mismatches	Indels 1	Gaps 1
Qy	QEPQSKA-RHGNTVPGEMPMQASVRRQGAHCSGLVADTIVTLAAHCFEKAATETLS	107		
Db	105 QRGPPRPQRENTVPGEMPMQASVRRQGAHCSGLVADTIVTLAAHCFEKAATETLS	164		
Qy	108 MSVVLGSLQREGLSPGAEEVGAALQQLPRAYNHVQSGSLALDLOLAHPTTHPLCLPPA	167		
Db	165 MSVVLGSLQREGLSPGAEEVGAALQQLPRAYNHVQSGSLALDLOLAHPTTHPLCLPPA	224		
Qy	168 HRFPFGASCMAATGMWQODTSDAPGTLRLRLISRPTNCIYNQLOHRLNSPARPGMLC	227		
Db	225 HRFPFGASCMAATGMWQODTSDAPGTLRLRLISRPTNCIYNQLOHRLNSPARPGMLC	284		
Qy	228 GGPQPGVQPCQSGDGGGVLCLPDPGHVWAQIISFASCAQEDAPVLLITNTAAISSMLQ	287		
Db	285 GGPQPGVQPCQSGDGGGVLCLPDPGHVWAQIISFASCAQEDAPVLLITNTAAISSMLQ	344		
Qy	288 ARVQGAFLAQSPETPPEMSDESDSCVACGSLRTAGVQAGAPSPWPEARIMHOGQLACGA	347		
Db	345 ARVQGAFLAQSPETPPEMSDESDSCVACGSLRTAGVQAGAPSPWPEARIMHOGQLACGA	404		
Qy	348 LVSEBAVLTAAHCFITGRQAPPEEWSVGLGTRPEEWGLKQILIHGAATTHEEGYDMLALLLA	407		
Db	405 LVSEBAVLTAAHCFITGRQAPPEEWSVGLGTRPEEWGLKQILIHGAATTHEEGYDMLALLLA	464		
Qy	408 QPVTIGASTIRPLCLFYPDDHNLPDGERGVNLGAPARQAGISSIQTVPVTLIGPACSRLLHA	467		

Db	465	QPTTLGASLRPLCLPYPDHLHPDGRGNVLGRARGAGTSSLSQTVPTLLGPRACSLHA	52
Oy	468	APGGDGSPIILPGWCTSAVAGELPSCGELSGAPLVHEVGTWFLAGLHSFGDACGPARPA	527
Db	525	APGGDGSPIILPGWCTSAVAGELPSCGELSGAPLVHEVGTWFLAGLHSFGDACGPARPA	584
Oy	528	VFTALPAYEDWWSLDMQVYFAEEEPPEAPESCLANISQPTSC	571
Db	585	VFTALPAYEDWWSLDMQVYFAEEEPPEAPESCLANISQPTSC	628
RESULT 7			
ABP72374	ID	ABP72374 standard; Protein; 642 AA.	
XX	XX	ABP72374;	
XX	AC	13-MAY-2003 (first entry)	
XX	DT		
XX	DE	Transmembrane serine protease 20 (MTSP20).	
XX	XX		
KW	Human; Transmembrane serine protease 20; MTSP20; enzyme;		
KW	endorphinase; cytosolic; dermatological; cardiac; vulnary;		
KW	ophthalmological; gene therapy.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
PH	Key	Location/Qualifiers	
FT	Peptide	1..24	
FT		/label= Signal_peptide	
FT	Protein	25..642	
FT		/label= Mature_protein	
FT	Domain	82..99	
FT		/note= "transmembrane domain"	
FT	Cleavage-site	112..113	
FT		/note= "protease activation cleavage site"	
FT	Domain	113..343	
FT		/note= "trypsin-like serine protease domain, specifically described in Claim 11"	
FT	Cleavage-site	375..376	
FT		/note= "protease activation cleavage site"	
FT	Domain	376..624	
FT		/note= "trypsin-like serine protease domain, specifically described in Claim 9"	
FT	Region	624..642	
FT		/note= "region specifically described in Claim 5"	
FT	Modified-site	77	
FT		/note= "potential N-glycosylation site"	
FT	Modified-site	621	
FT		/note= "potential N-glycosylation site"	
XX	PN	WO2003004681-A2.	
XX	XX		
PD	16-JAN-2003.		
XX	XX		
PF	03-JUL-2002; 2002WO-US21208.		
XX	XX		
PR	03-JUL-2001; 2001US-302939P.		
PA	(CORV-) CORVAS INT INC.		
XX	XX		
PI	Madison EL, Ong EO;		
XX	XX		
DR	WPI: 2003-239207/23.		
XX	DR	N-PSDB; ABZ58499.	
XX	XX		
PT	New type-II membrane-type serine protease 20 polypeptides, useful for		
PT	preparing a medicament for diagnosing, treating or preventing cancer,		
PT	dermatological disorders, aberrant wound repairs or crest syndromes -		
XX	XX		
PS	Claim 5; Page 212-213; 216pp; English.		
XX	XX		

Key	Location/Qualifiers
Peptide	1..24
Protein	/label= Signal_peptide 25..642
Domain	/label= Mature_protein 82..99
Cleavage-site	/note= "transmembrane domain" 112..113
Domain	/note= "protease activation cleavage site" 113..343
Cleavage-site	/note= "trypsin-like serine protease domain, specifically described in Claim 11" 375..376
Domain	/note= "protease activation cleavage site" 376..624
Region	/note= "trypsin-like serine protease domain, specifically described in Claim 9" 624..642
Modified-site	/note= "region specifically described in Claim 5" 77
Modified-site	/note= "potential N-glycosylation site" 621
Modified-site	/note= "potential N-glycosylation site"
WO2003004681-A2.	
16-JAN-2003.	
03-JUL-2002; 2002MC-US21208.	
03-JUL-2001; 2001US-302939F.	
(CORV-) CORVAS INT INC.	
Madison EL, Ong EO.	
WPI; 2003-239207/23.	
N-PSDB; ABZ58499.	
New type-II membrane-type serine protease 20 polypeptides, useful for preparing a medicament for diagnosing, treating or preventing cancer, dermatological disorders, aberrant wound repairs or crest syndromes -	
Claim 5; Page 212-213; 216pp; English.	

The present sequence is the protein sequence of novel human type II transmembrane serine protease 20 (MSP20), an endothelial cell transmembrane protein (endothelase) that is expressed in oesophageal tumour tissues, in lung carcinoma, colon, cervix, leukaemia and other cell lines as well as in certain healthy cells and tissues. The level of MSP20 can be diagnostic of prostate, uterine, lung, oesophagus or colon cancer, or leukaemia. The expression and/or activation of MSP20 on, or in the vicinity of, a cell or a bodily fluid can be a marker for breast, prostate, lung, colon and other cancers. The invention provides MSP20 polypeptides and protease domains, zymogen and activated forms, single and multi chain forms, the nucleic acids encoding them, probes and primers, expression vectors, host cells, antibodies and transgenic animals. Nucleic acids encoding MSP20 or its protease domain can be expressed in a host cell, and the protein used in assays to identify candidate compounds that modulate MSP activity. A claimed method of inhibiting tumour initiation, growth or progression or for treating a malignant or pre-malignant condition, especially of the breast, cervix, prostate, lung, ovary or colon, involves administering an inhibitor of a MSP20 polypeptide, especially an antisense oligonucleotide, double-stranded RNA or antibody (all claimed). These inhibitors are also used in a claimed method of treating or preventing a disease or disorder associated with undesired and/or uncontrolled angiogenesis or neovascularisation, especially undesired angiogenesis associated with solid neoplasms, vascular malformations and cardiovascular disorders (especially angiodysplasia, angiolipoma, atherosclerosis, restenosis/reperfusion injury, arteriovenous malformations, haemangiomatosis and vascular adhesion, dyschondroplasia with vascular hamartoma (Falcucci's syndrome), hereditary haemorrhagic telangiectasia (Rendu-Osler-Weber syndrome) and von Hippel Lindau syndrome), chronic inflammatory diseases (especially diabetes mellitus, haemophilic joints, inflammatory bowel disease, nonhealing fractures, periodontitis, psoriasis, rheumatoid arthritis, venous stasis ulcers, granuloma-in-burns, hypertrophic scars, liver cirrhosis, osteoradionecrosis, postoperative adhesions, pyogenic granuloma and systemic sclerosis), aberrant wound repairs, circulatory disorders (especially Raynaud's phenomenon), crest syndromes (especially calcinosis, oesophageal, myomectomy), sclerodactyly and telangiectasis), dermatological disorders (especially systemic vasculitis, scleroderma, pyoderma gangrenosum, vasculopathy, venous, arterial ulcers, Sturge-Weber syndrome, Post-wine stains, blue rubber bleb naevus syndrome, Klippel-Trenaunay-Weber syndrome and Osler-Weber-Rendu syndrome) and ocular disorders (especially blindness caused by ocular neovascular disease, corneal graft neovascularisation, macular degeneration in the eye, neovascular glaucoma, trachoma, diabetic retinopathy, myopic degeneration, retinopathy of prematurity, retrolental fibroplasia and corneal neovascularisation).

Sequence 642 AA:

Query Match 89.4%; Score 2779.5; DB 24; Length 642;

Best Local Similarity 98.5%; Pred. No. 1.7e-184; Matches 511; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

49 OSEPOGAK-RHGNTVGEWPMOASVRGCAHICSGSLVADTWLTAHCFEKAATELNS 107
 105 QGQGPPEKQEGNTVGEWPMOASVRGCAHICSGSLVADTWLTAHCFEKAATELNS 164
 108 MSVLGSLQREGSLPAGAEVVAALQLPRAVNHYSOGSLALQLAHPTTHPLCLPQA 167
 165 MSVLGSLQREGSLPAGAEVVAALQLPRAVNHYSOGSLALQLAHPTTHPLCLPQA 224
 168 HRPFGASCAWATGWDOTSDAPGTLNLRLISRTCCNYINQLHQRHLSNPARPGLC 227
 225 HRPFGASCAWATGWDOTSDAPGTLNLRLISRTCCNYINQLHQRHLSNPARPGLC 284
 228 GGPFGVQPGCGGSGPVLCLEPDGHWVAGIISFASCAQEDPAVLLTNTAAHSWIO 287
 285 GGPFGVQPGCGGSGPVLCLEPDGHWVAGIISFASCAQEDPAVLLTNTAAHSWIO 344

288 ARVQGAFLAOSPETPEMSDSDSCVACGSLRTAGQQAAPSPWPPEARLHMGOGLACGA 347
 345 ARVQGAFLAOSPETPEMSDSDSCVACGSLRTAGQQAAPSPWPPEARLHMGOGLACGA 404
 348 LVSEBAVLTAAACFTGPRAPAEWSVGLGTRPEMGLKQILHGAATHPGCGDMLLLLA 407
 405 LVSEBAVLTAAACFTGPRAPAEWSVGLGTRPEMGLKQILHGAATHPGCGDMLLLLA 464
 408 QPVLGASLRPLCLDPDHLPDGERGWLGRAPDAGISSIQTVPTLLGPRACRLHA 467
 465 QPVLGASLRPLCLDPDHLPDGERGWLGRAPDAGISSIQTVPTLLGPRACRLHA 524
 468 AFGGGSPLPDMWCTSAVGEIPSCGSLGAPLVHEVGTWTLAHSFGDACCQPARPA 527
 525 AFGGGSPLPDMWCTSAVGEIPSCGSLGAPLVHEVGTWTLAHSFGDACCQPARPA 584
 528 VFTALPAYEDWVSSLDMOVYFAEPEPEAPEPCSCIANIS 566
 585 VFTALPAYEDWVSSLDMOVYFAEPEPEAPEPCSCIANIS 623

RESULT 8

ID AAE21440 standard; Protein; 552 AA.

AAE21440;

16-JUL-2002 (first entry)

Human m32404 protein.

Human; trypsin; m32404 protein; bone disorder; osteoporosis; osteopenia; tropical sprue; immune disorder; cellular proliferative disorder; asthma; psoriasis; allergy; carcinoma; leukaemia; hematopoietic disorder; liver disorder; sarcoma; cardiovascular disorder; valvular disease; arrhythmia; cardiomyopathy; viral disease; pain; metabolic disorder; vaccine; gene therapy; protein therapy; cytoskeletal; immunomodulatory; virucide; analgesic; enzyme.

Homo sapiens.

WO200226802-A2.

04-APR-2002.

24-SEP-2001; 2001WO-US29904.

25-SEP-2000; 2000US-235023P.

(MILL-) MILLENNIUM PHARM INC.

Meyers RA;

WPI. 2002-315795/35.

N-PSDB; AAD33878.

Nucleic acids encoding human trypsin m32404, useful for preventing diagnosing and treating e.g. bone disorders, cellular proliferative disorders and immune disorders -

Claim 5; Page 114; 125pp; English.

The present invention relates to human trypsin designated m32404 proteins and polynucleotides encoding such proteins. m32404 sequences are useful in the prevention, diagnosis and treatment of diseases associated with inappropriate m32404 trypsin expression. They are used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of m32404 trypsin by expressing inactive proteins or to supplement the patients own production of m32404 trypsin. They are also used to prevent, diagnose and/or treat bone disorders (e.g. osteoporosis, osteopenia, tropical sprue), immune disorders (e.g. psoriasis, asthma, allergies), cellular proliferative disorders (e.g. carcinoma, sarcoma and leukaemia), hematopoietic

disorders, liver disorders, cardiovascular disorders (e.g. valvular diseases, arrhythmias and cardiomyopathies), viral diseases, pain and/or metabolic disorders. Sequences of the invention are used as vaccines. They are also used in gene therapy and protein therapy. The present sequence is human m32404 protein.

Sequence 552 AA:

Query Match 74.1%; Score 2304; DB 23; Length 552;

Best Local Similarity 80.7%; Pred. No. 1.3e-151;

Matches 421; Conservative 26; Mismatches 69; Indels 6; Gaps 2;

```

OY 50 EPQGAHAKHNTVPEPMWQASVRQGAHICGSLVADTWVLTAAHCEKAATLNSWS 109
DB 37 EPO-----EGNTLPEPMWQASVRQGVHICGSLVADTWVLTAAHCEKAATLNSWS 91
OY 110 VLGLSLOREGSLPGEAEVVALQCPRAYNHYSQGSDDLALQAPTHHTPLCLPQPAHR 169
DB 92 VLGLSLKQEGQSPGAEVVALQCPRAYNHYSQGSDDLALQAPTHHTPLCLPQPAHR 151
OY 170 FPFGASCMATGMDQDTPADPGLTNRRLRLISRPTCNQIYNQHQHNSNPARPGMLCGG 229
DB 152 FPFGASCMATGMDQDTPADPGLTNRRLRLISRPTCNQIYNQHQHNSNPARPGMLCGG 211
OY 230 PPGVQGPCCGDSGPVCLPEPDGHWVQAGTISFASCAQEDAPVLLTNTAAHSSWLGAR 289
DB 212 AOPGQGGCCGDSGPVCLPEPDGHWVQAGTISFASCAQEDAPVLLTNTAAHSSWLGAR 271
OY 290 VQGAFLASPEPTPMSEDSQVACGSLRTAGPQAGSPWMEARLMHOGQLACGALV 349
DB 212 VHEAFLVQAPFVVMSPDENSQVACGSLRTAGPQAGSPWMEARLMHOGQLACGALV 331
OY 350 SEEAVALTAHCFIQHAEPEWSVGLGTRPEEWGLKQLIHGAYTHPEGGYDMALLLQAP 409
DB 332 SEVVVLTAAHCFIQHAEPEWSVGLGTRPEEWGLKQLIHGAYTHPEGGYDMALLLQAP 391
OY 410 VTGASLRPLCLPYDHLPDGERGWLGRAPGAGISSLOTVPVTLGPRACSLHAAP 469
DB 392 VTIGLGRPLCLPYDHLPDGERGWLGRAPGAGISSLOTVPVTLGPRACSLHAAP 450
OY 470 GGDGSPILPGWCTSAVGELESCGSLGAPLVHEVYRGVWFLAGLSFGDACCGPARPAVF 529
DB 451 GGTGPIPLPGWCTTVGEPPHCEGLSGAPLVHEIRGTWFLVGLHSFGDTCOSAKPAVF 510
OY 530 TALPAYEDWVSLDWQVFAEEPEPEAPGSCLANISOPTSC 571
DB 511 AALSAYEDWISLWQVFAEEPEPEATGSCLVNSQPASC 552

```

RESULT 9

AA90291 ID AAY90291 standard; Protein; 267 AA.

AC AAY90291;

DT 24-OCT-2000 (first entry)

DE Human peptidase, HPEP-8 protein sequence.

Human; peptidase; cell proliferative disorder; arteriosclerosis; psoriasis; myelofibrosis; cancer; autoimmune disorder; Crohn's disease; inflammatory disorder; AIDS; anaemia; allergy; asthma; atherosclerosis; Grave's disease; multiple sclerosis; scleroderma; infection; diabetes; metabolic disorder; Addison's disease; cystic fibrosis; diagnosis; glycogen storage disease; obesity; therapy; HPEP-8.

OS Homo sapiens.

PN WO200042201-A2.

XX 20-JUL-2000.

PF 11-JAN-2000; 2000MO-US00641.

XX 11-JAN-1999; 99US-0172247.
PR 03-MAY-1999; 99US-0132253.
PR 27-MAY-1999; 99US-0136653.

XX (INCY-) INCYTE PHARM INC.

PI Bandman O, Hillman JL, Tang YT, Azimzai Y, Baughn MR, Lal P;

PI Yue H, Lu DAM;

DR MPI; 2000-482832/42.

DR N-P8DB; AAA37664.

PR An isolated polypeptide for diagnosis, prevention and treatment of

PT cell proliferative, autoimmune/ inflammatory and metabolic disorders

PS comprises a sequence encoding a human peptidase -

CC This sequence represents a human peptidase, designated HPEP-8. The

CC invention relates to 18 human peptidases designated HPEP-1 to HPEP-18,

CC respectively. The peptidases can be used for treating a disease or

CC condition associated with decreased expression or over expression of

CC functional human peptidases. The diseases that can be diagnosed,

CC prevented and treated include cell proliferative disorders (such as

CC arteriosclerosis, psoriasis, myelofibrosis, and cancers),

CC autoimmune/inflammatory disorders (such as AIDS, anaemia, allergies,

CC Crohn's disease, asthma, atherosclerosis, Grave's disease, multiple

CC sclerosis, and scleroderma), infections, and metabolic disorders (such as

CC Addison's disease, diabetes, cystic fibrosis, glycogen storage diseases

CC and obesity).

XX Sequence 267 AA;

Query Match 46.8%; Score 1454; DB 21; Length 267;

Best Local Similarity 99.6%; Pred. No. 4.8e-93;

Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 305 MSDESCVACGSLRTAGPQAGAPSPWMEARLMHOGQLACGALVSEBAVLTAHCFIQR 364

DB 1 MSDESCVACGSLRTAGPQAGAPSPWMEARLMHOGQLACGALVSEBAVLTAHCFIQR 60

OY 365 QAPEWMSVGLGTRPEEWGLKQLIHGAYTHPEGGYDMALLLQAPVTLGASLRPLCLPY 424

DB 61 QAPEWMSVGLGTRPEEWGLKQLIHGAYTHPEGGYDMALLLQAPVTLGASLRPLCLPY 120

OY 425 DHHLPDGERGWLGRAPGAGISSLOTVPVTLGPRACSLHAAPGSGSPILPGMCTS 484

DB 121 DHHLPDGERGWLGRAPGAGISSLOTVPVTLGPRACSLHAAPGSGSPILPGMCTS 180

OY 485 AVGELPSCGELSGAPLVHEVYRGVWFLAGLSFGDACCGPARPAFTALPAEDWVSSLDW 544

DB 181 AVGELPSCGELSGAPLVHEVYRGVWFLAGLSFGDACCGPARPAFTALPAEDWVSSLDW 240

OY 545 QVYFAEEPEPEAPGSCLANISOPTSC 571

DB 241 QVYFAEEPEPEAPGSCLANISOPTSC 267

RESULT 10

AA20156 ID AAB20156 standard; Protein; 267 AA.

AC AAB20156;

DT 30-APR-2001 (first entry)

DE Human protein SECP2.

XX SECP2; secreted protein; human; diagnosis; therapy.

XX Homo sapiens.

PN WO200105971-A2.
 XX
 XX 25-JAN-2001.
 XX
 PF 20-JUL-2000; 2000WO-US19890.
 XX
 XX 20-JUL-1999; 99US-0144722.
 PR 29-NOV-1999; 99US-0167785.
 PR 19-JUL-2000; 2000US-0619252.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Fernandes E;
 DR WPI; 2001-091973/10.
 DR N-PSDB; AAF30189.
 XX
 PT New polypeptide designated SECP, its encoding nucleic acid and its
 PT immunospecific antibody, useful for diagnosing, preventing and treating
 PT SECP-associated disorders such as cancer -
 XX
 PS Claim 1; Fig 2; 124pp; English.
 XX
 CC The present sequence is that of novel human protein SECP2,
 CC which is predicted to localise in the microbody (peroxisome),
 CC and which does not appear to include a signal peptide. The
 CC protein shows homology to human PRO351 protein, and to a region
 CC of human prostatic precursor. The invention provides 9 novel
 CC SECP proteins (see AAB20155-63), nucleic acids encoding them
 CC (see AAF30188-96), antibodies, mutants or fragments. These can
 CC be used to detect, treat or prevent an SECP-associated disorder,
 CC to screen for predisposition to such a disorder, and to identify
 CC agents that modulate the expression or activity of SECP.
 CC
 SQ Sequence 267 AA;
 Query Match 46.2%; Score 1436; DB 22; Length 267;
 Best Local Similarity 98.9%; Pred. No. 8.4e-92;
 Matches 264; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 305 MSDEDSVAGCSLRTAGPAGAPSPMPWEARLMHOGQLVSEAVLTAHGFGR 364
 DB 1 MSDEDSVAGCSLRTAGPAGAPSPMPWEARLMHOGQLVSEAVLTAHGFGR 60
 QY 365 QAPPEWSVGLGTPEEWMGKOLLHGAATYHPEGGYDMLLLAOPVTLGASRLPLCLPP 424
 DB 61 QAPPEWSVGLGTPEEWMGKOLLHGAATYHPEGGYDMLLLAOPVTLGASRLPLCLPP 120
 QY 425 DHHLPGERGWLGRARPGAGISSLOTVPVTLIGPACSRRLHAAPGCGSPILPGWCTS 484
 DB 121 DHHLPGERGWLGRARPGAGISSLOTVPVTLIGPACSRRLHAAPGCGSPILPGWCTS 180
 QY 485 AVGELPSCGSLGAPLVHEVRGTFAGHSFGDACCQPARPVFALPAVEDWWSLDM 544
 DB 181 AVGELPSCGSLGAPLVHEVRGTFAGHSFGDACCQPARPVFALPAVEDWWSLDM 240
 QY 545 QVYFAEPPEPEAPSPGCLANISQPTSC 571
 DB 241 QVYFAEPPEPEAPSPGCLANISQPTSC 267
 RESULT 11
 AAB72373
 ID AAB72373 standard; Protein; 267 AA.
 AC AAB72373;
 XX
 XX 13-MAY-2003 (first entry)
 XX
 XX Transmembrane serine protease 20 (MTSP20) protease domain.
 DE
 XX
 XX Human; transmembrane serine protease 20; MTSP20; enzyme;
 KW endotheliasae; cytosolic; dermatological; cardiant; vulnery;

KW ophthalmological; gene therapy.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2003004681-A2.
 PN
 XX
 XX 16-JAN-2003.
 PD
 XX
 PF 03-JUL-2002; 2002WO-US21208.
 XX
 PR 03-JUL-2001; 2001US-302939P.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 PI Madison EL, Ong EO;
 XX
 XX WPI; 2003-239207/23.
 DR N-PSDB; ABE58498.
 XX
 PT New type-II membrane-type serine protease 20 polypeptides, useful for
 PT preparing a medicament for diagnosing, treating or preventing cancer,
 PT dermatological disorders, aberrant wound repairs or crest syndromes -
 XX
 PS Claim 5; Page 204-205; 216pp; English.
 XX
 CC The present sequence is the protein sequence of protease domain 2
 CC of novel human type II transmembrane serine protease 20 (MTSP20).
 CC MTSP20 (see also AAB72374) is an endothelial cell transmembrane
 CC protein (endotheliasae) that is expressed in oesophageal tumour
 CC tissues, in lung carcinoma, colon, cervix, leukaemia and other
 CC cell lines as well as in certain healthy cells and tissues. The
 CC level of MTSP20 can be diagnostic of prostate, uterine, lung,
 CC oesophagus or colon cancer, or leukaemia. The expression and/or
 CC activation of MTSP20 on, or in the vicinity of, a cell, or a
 CC bodily fluid can be a marker for breast, prostate, lung, colon and
 CC other cancers. The invention provides MTSP20 polypeptides and
 CC protease domains, zymogen and activated forms, single and multi
 CC chain forms, the nucleic acids encoding them, probes and primers,
 CC expression vectors, host cells, antibodies and transgenic animals.
 CC Nucleic acids encoding MTSP20 or its protease domain can be
 CC expressed in a host cell, and the protein used in assays to identify
 CC candidate compounds that modulate MTSP activity. A claimed method
 CC of inhibiting tumour initiation, growth or progression or for
 CC treating a malignant or pre-malignant condition, especially of the
 CC breast, cervix, prostate, lung, ovary or colon, involves
 CC administering an inhibitor of a MTSP20 polypeptide, especially an
 CC antisense oligonucleotide, double-stranded RNA or antibody (all
 CC claimed). These inhibitors are also used in a claimed method of
 CC treating or preventing a disease or disorder associated with
 CC undesired and/or uncontrolled angiogenesis or neovascularisation,
 CC especially undesired angiogenesis associated with solid neoplasms,
 CC vascular malformations and cardiovascular disorders (especially
 CC angiolipoma, angiolipoma, atherosclerosis, restenosis/reperfusion
 CC injury, arteriovenous malformations, haemangiomas and vascular
 CC adhesion), dyschondroplasia with vascular hamartoma (Fatucci's
 CC syndrome), hereditary haemorrhagic telangiectasia
 CC (Rendu-Osler-Weber syndrome) and von Hippel Lindau syndrome),
 CC chronic inflammatory diseases (especially diabetes mellitus,
 CC haemophilic joints, inflammatory bowel disease, nonhealing
 CC fractures, periodontitis, psoriasis, rheumatoid arthritis, venous
 CC stasis ulcers, granulatois-burns, hypertrophic scars, liver
 CC cirrhosis, osteoradionecrosis, postoperative adhesions, pyogenic
 CC granuloma and systemic sclerosis), aberrant wound repairs,
 CC circulatory disorders (especially Raynaud's phenomenon), crest
 CC syndromes (especially calcinosis, oesophageal, dyomectocly,
 CC sclerodactyly and telangiectasis), dermatological disorders
 CC (especially systemic vasculopathy, venous, arterial ulcers,
 CC gangrenosum, vasculopathy, venous, pyoderma
 CC Sturge-Weber syndrome, Post-wine stains, blue rubber bleb naevus
 CC syndrome, Klippel-Trenaunay-Weber syndrome and Osler-Weber-Rendu
 CC syndrome) and ocular disorders (especially blindness caused by
 CC ocular neovascular disease, corneal graft neovascularisation,
 CC macular degeneration in the eye, neovascular glaucoma, trachoma,

CC diabetic retinopathy, myopic degeneration, retinopathy of
CC prematurity, retrolental fibroplasia and corneal
CC neovascularisation).

SQ Sequence 267 AA;

Query Match	43.3%	Score	1346	DB 24	Length	267
Best Local Similarity	98.8%	Pred.	No. 1.5e-85			
Matches 245	Conservative	1	Mismatches	2	Indels	0
					Gaps	0

QY	319	TAPRQAGASPMWMEARLHHQOLACGGALVSEEVLTAAHCFGRQAPREWSVSGITSP	378
Db	1	TAPRQAGASPMWMEARLHHQOLACGGALVSEEVLTAAHCFGRQAPREWSVSGITSP	60
QY	379	EEWGLKQILHGAVTPEGGYDMALLLAQVTLGASLRPLCLPYRDHNLPRDGGEGWVLG	438
Db	61	EEWGLKQILHGAVTPEGGYDMALLLAQVTLGASLRPLCLPYRDHNLPRDGGEGWVLG	120
QY	439	RARGAGISLQVTPVTLTGPRACSTLHAAPGGDSSPLLPRMVTCSANGLPSPSEGISGA	498
Db	121	RARGAGISLQVTPVTLTGPRACSTLHAAPGGDSSPLLPGMVTCSANGELPSPSEGISGA	180
QY	499	PLVHEVRGTWFLAGLHSPGDACGAPRAVFTALPAYEDWSSLDWQYFAEEPEPEAP	558
Db	181	PLVHEVRGTWFLAGLHSPGDACGAPRAVFTALPAYEDWSSLDWQYFAEEPEPEAP	240
QY	559	GSCLANIS 566	
Db	241	GSCLANIS 248	

RESULT 12
AAB20162
ID AAB20162 standard; Protein; 198 AA

AC AAB20162;

DT 30-APR-2001 (first entry)

Human protein SECP8.

SECP8; secreted protein; human; diagnosis; therapy

OS · Homo sapiens.

PN WO200105971-A2.

PD 25-JAN-2001

PF 20-JUL-2000; 2000WO-US19890.

PR 20-JUL-1999; 99US-0144722

PR 19-JUL-2000; 2000US-0619252

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Fernandes E;
vxy

DR WPI; 2001-091973/10
DP N-PSDB; AAE30195

XX PT New polymeride des:

PT immunospecific anti-
PT SECP-associated diso

PS Claim 1; Fig 8; 124pp; English.

CC The present sequence is that of novel human protein SECP8

CC which is predicted to localise in the cytoplasm, and which does
CC not appear to include a signal peptide. The invention provides 9
CC novel SECP proteins (see AAB20155-63), nucleic acids encoding them
CC (see AAF30188-96), antibodies, mutants or fragments. These can

CC be used to detect, treat or prevent an SECP-associated disorder,
CC to screen for predisposition to such a disorder, and to identify
CC agents that modulate the expression or activity of SECP.

SQ Sequence 198 AA;

Query March	32.9%	Score 1023	DB 22	Length 198
Best Local Similarity	99.5%	Pred. No. 2.6e-63		
Matches 188	0	Mismatches 1	Indels 0	Gaps 0
Conservative				

Qy	303	MSDESDCVACGSLRTTNGPAGAPSPWMPPEARLIMHQGLACGGALVSEBAVLTAAHCITGR	364
Db	1	MSDESDCVACGSLRTTNGPAGAPSPWMPPEARLIMHQGLACGGALVSEBAVLTAAHCITGR	60
Qy	365	QAPBEEMSVGLGRPREEMGKLQILHGATVTHEGGYDMLLLLAQPVTLGASLRPLCLPYR	424
Db	61	QAPBEEMSVGLGRPREEMGKLQILHGATVTHEGGYDMLLLLAQPVTLGASLRPLCLPYR	120
Qy	425	DHHLPGERGMVLGRARPAGISSLQTYPVTLIGPRACSLHAAPOGDGSEILPGMWCTS	484
Db	121	DHHLPGERGMVLGRARPAGISSLQTYPVTLIGPRACSLHAAPOGDGSEILPGMWCTS	180
Qy	485	AVGELPSCE	493
Db	181	AVGELPSCE	189

RESULT 13
AAV72095
ID AAV72095 standard; Protein; 219 AA

AC AAY72095;

DT 28-MAR-2001 (first entry)

DE Human serine protease #6 encoded by clone HTTJk57.

Human, serine protease, osteopathic, immunosuppressive, antiallergic;
antihistaminic; cytostatic; cardiatic; neuroprotective; nootropic;
neuroinflammatory; cytotoxic; ophthalmological; antibacterial; antiviral;
antifungal; antiparasitic; gene therapy; diagnosis; prevention; glaucoma;
treatment; bone formation disorder; autoimmune disorder; arthritis; cancer;
connective tissue disorder; autoimmunity disorder; wound healing; asthma;
systemic lupus erythematosus; male reproductive system disorder;
testicular cancer; digestion and food absorption disorder; arrhythmia;
Crohn's disease; neurodegenerative disease; Alzheimer's disease; allergy
behavioral disorder; Tourette's syndrome; acute myelogenous leukaemia;
cardiovascular disorder; ocular disorder; drug screening.

OS Homo sapiens.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
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99	99	99
100	100	100

	/note= "Immunogenic epitope"
FT	70 75
EE	
Posit	

FT	/label= Histidine_active_site_domain
FT	115 123

Region	Immunogenic epitope
158	167

FT	Region	/note= "Immunogenic epitope"
FT	190-202	

```

/notice= "Immunogenic epitope
FI
XX

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MOZ0006824/-AZ
FN
XX

[illegible]

XX	8
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	1
	6
	9
	4
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	3
	6
	6
	1
	4
	1
	6

PR 20-MAY-1999; 99US-0135163

PR 09-SEP-1999; 99US-0152935.

PR 01-NOV-1999; 99US-0162979.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Shi Y, Young PE, Ni J;
XX MPI: 2000-679799/66.
XX N-PSDB; AAD02325.
XX
XX New nucleic acid molecules encoding human serine protease polypeptides,
XX useful for diagnosis, prevention and/or treatment of disorders e.g.
XX osteoporosis, lupus erythematosus and Alzheimer's -
XX
XX Claim 12; Page 282-283; 289pp; English.
XX
XX The present sequence is human serine protease #6 from clone
XX HTK57 (ATCC Deposit No: PTA538).
XX The invention relates to human serine proteases and their cDNA clones.
XX It is used in methods for the diagnosis, prevention and treatment of
XX various disorders related to serine protease such as bone formation
XX disorders (osteoporosis), connective tissue disorders (arthritis),
XX autoimmune disorders (systemic lupus erythematosus), wound healing, male
XX reproductive system disorders (testicular cancer), digestion and food
XX absorption disorders (Crohn's disease), neurodegenerative diseases
XX (Alzheimer's disease), behavioral disorders (Tourette's syndrome),
XX proliferative and cancerous conditions (acute myelogenous leukaemia),
XX allergic reactions (asthma), cardiovascular disorders (arthritis),
XX ocular disorders (glaucoma) and infectious diseases caused by bacteria,
XX viruses, fungi or parasites. It is also useful for screening therapeutic
XX compounds. Serine proteases are used as immunological probes or
XX polymorphic markers for the identification of chromosomes, cells and
XX tissues in biological samples, identification of male contraceptive
XX agents, delivery of compositions to targeted cells expressing a
XX receptor for serine protease, hybridization probes and molecular weight
XX markers. Serine protease nucleic acids are also useful in gene therapy.
XX Note: The present sequence shown in page 282-283 of sequence listing has
XX been assigned SEQ ID NO: 16. But the sequence, peptide fragment #14
XX related to human serine protease (AAV72117) shown in page 15 is also
XX referred as SEQ ID NO: 16.
XX
XX Sequence 219 AA:
SQ
Query Match 32.3%; Score 1003.5; DB 21; Length 219;
Best Local Similarity 95.8%; Pred. No. 6,5e-62;
Matches 184; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
QY 49 GEPQKAK-RHGNTPGEMWQASVRQGAHICSGSLVADTWLTAHCFEKAATELNS 107
DB 27 QRGPPKPKQBSGVTFGEWPMQASVRQGAHICSGSLVADTWLTAHCFEKAATELNS 86
QY 108 WSVVLGSLQREGLSPGAEEVGAALQLPRAVNHYSQSGDLALLQLAHPHTHTPLCLPPA 167
DB 87 WSVVLGSLQREGLSPGAEEVGAALQLPRAVNHYSQSGDLALLQLAHPHTHTPLCLPPA 146
QY 168 HRPFGASCWATGMDOTSDAPGTLRNLRLISRTNCIYNQHLHRLSNPARGMLC 227
DB 147 HRPFGASCWATGMDOTSDAPGTLRNLRLISRTNCIYNQHLHRLSNPARGMLC 206
QY 228 GGPQGVQSGPCQ 239
DB 207 GGPQGVQSGPCQ 218
RESULT 14
AAG67515
ID AAG67515 standard; Protein; 301 AA.
XX AAG67515;
XX
XX 26-NOV-2001 (first entry)
XX
XX Amino acid sequence of a human secreted polypeptide.

KM Human; secreted polypeptide; nervous disease; muscular disease; tumour;
KM gastrointestinal ulceration; spinal cord disease; trachea disease;
KM thyroid gland disease; ovary disease; prostate disease; heart disease;
KM renal gland disease; small intestine disease; thymus disease;
KM lymph node disease; muscular system disease; colon disease;
KM lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
KM myocardial infarction; angioplasty; liver disease; coagulation disorder;
KM microbial disease; immune disorder; inflammation; transplant rejection;
KM bone thickness; bone density; ferroxiadase loss; apoptosis;
KM vascular smooth cell proliferation; vaccine.
XX
XX Homo sapiens.
XX
XX WO200166690-A2.
XX
XX 13-SEP-2001.
XX
XX PD
XX
XX 05-MAR-2001; 2001WO-US07143.
XX
XX 06-MAR-2000; 2000US-0187107.
XX 13-MAR-2000; 2000US-0188916.
XX 03-OCT-2000; 2000US-0236874.
XX 03-OCT-2000; 2000US-0237846.
XX
XX (SMK) SMITHKLINE BEECHAM CORP.
XX (SMK) SMITHKLINE BEECHAM PLC.
XX
XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX MPI: 2001-570768/64.
XX N-PSDB; AAH78207.
XX
XX Novel isolated secreted polypeptide useful for treating nervous and
XX muscular diseases, gastrointestinal ulceration, coagulation and immune
XX disorders, microbial diseases, inflammation and transplant rejection -
XX
XX Claim 1; Page 74-75; 102pp; English.
XX
XX The present sequence represents a human secreted polypeptide. The
XX secreted polypeptides and polynucleotides are useful for treating
XX nervous and muscular diseases, for inhibiting tumour formation and
XX metastasis, for treating gastrointestinal ulceration, for preventing
XX and treating diseases in spinal cord, thyroid gland, ovary, prostate,
XX renal gland, small intestine, heart, trachea, thymus, lymph node,
XX muscular system and colon, for treating lipase deficiency in cystic
XX fibrosis and pancreatitis, for treating undesirable clot formation
XX such as myocardial infarction, during angioplasty and all surgical
XX procedures that require decreased blood clot formation, for treating
XX liver diseases, coagulation disorders and microbial diseases, for
XX treating immune disorders, for treating inflammation and transplant
XX rejection, for enhancing bone thickness and increasing bone density,
XX for reducing the loss of essential ferroxiadases, for suppressing
XX apoptosis, and for regulating vascular smooth cell proliferation. They
XX may also be used as vaccines.
XX
XX Sequence 301 AA:
SQ
Query Match 28.8%; Score 896.5; DB 22; Length 301;
Best Local Similarity 38.3%; Pred. No. 2,4e-54;
Matches 199; Conservative 10; Mismatches 44; Indels 26; Gaps 6;
QY 53 GKAKHGNTVGEWPMQASVRQGAHICSGSLVADTWLTAHCFEKAATELNSWSV 111
DB 24 GKAPR-----PGAWMEQAVWPGSRPGHGLVSESWLAPASCTLEQVTHLCCRMTR 78
QY 112 LGSLOREGLSPG--AAEVGAALQLPRAVNHYSQSGDLALLQLAHPHTHTPLCLPPA 168
DB 79 VGAPFARRRGPGFWLESETFPVAVYLPRAVNHYSQSGDLALLQLAHPHTHTPLCLPPA 138
QY RPPFGASCWATGMDOTSDAPGTLRNLRLISRTNCIYNQHLHRLSNPARGMLC 228
DB 139 RPPFGASCWATGMDOTSDAPGTLRNLRLISRTNCIYNQHLHRLSNPARGMLC 198

```

QY 229 GPOGVGPGCGDGGSPVLCLEPDGHWVQAGIISFASCAQEDAPVLLTNTAAHSMWLOA 288
    |||||
Db 199 GPOGVGPGCG----- 209
QY 289 RVQGAFLAQSPTPEMSDESDCVACSLRTAGPQAGAPSPWPWEARLMHQGLACGAL 348
    |||||
Db 210 ----- 209
QY 349 VSEAVLTAHCFIGRQAPPEWSVGLGTRPEEMGLKOLIHGAYTHPEGYDMALLLQAQ 408
    |||||
Db 210 ----- 209
QY 409 PVTLGASLRPLCLPYPDHHLDPGERGWLGRARPAGAGISLOTVPVTLGPRACSLHAA 468
    |||||
Db 210 ----- 209
QY 469 PGDGSPIPLPGWCTSAVAGELPSCGSLGAPLVHEVRGTWFLAGHSFGDACQGPAPPAV 528
    |||||
Db 210 ----- 244
QY 529 FTALPAYEDWVSSLDW--QVYFAEPPEPEAPGSCLANIS 566
    |||||
Db 245 FTALPAYE--TGSVAVTRQVYFAEPPEPEAPGSCLANIS 282

```

RESULT 15
AAG67514
ID AAG67514 standard; Protein; 255 AA.

AC AAG67514;

DT 26-NOV-2001 (first entry)

DE Amino acid sequence of a human secreted polypeptide.

XX Human; secreted polypeptide; nervous disease; muscular disease; tumour;
 XX gastrointestinal ulceration; spinal cord disease; trachea disease;
 XX thyroid gland disease; ovary disease; prostate disease; heart disease;
 XX renal gland disease; small intestine disease; thymus disease;
 XX lymph node disease; muscular system disease; colon disease;
 XX lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
 XX myocardial infarction; angiodysplasia; liver disease; coagulation disorder;
 XX microbial disease; immune disorder; inflammation; transplant rejection;
 XX bone thickness; bone density; ferrooxidase loss; apoptosis;
 XX vascular smooth cell proliferation; vaccine.

OS Homo sapiens.

PN WO200166690-A2.

PD 13-SEP-2001.

PE 05-MAR-2001; 2001WO-US07143.

PR 06-MAR-2000; 2000US-0187107.

PR 13-MAR-2000; 2000US-0188916.

PR 03-OCT-2000; 2000US-0236874.

PR 03-OCT-2000; 2000US-0237846.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

DR WPI: 2001-570768/64.

DR N-PSDB; AAR78206.

XX Novel isolated secreted polypeptide useful for treating nervous and
 XX muscular diseases, gastrointestinal ulceration, coagulation and immune
 XX disorders, microbial diseases, inflammation and transplant rejection -
 PS Claim 1; Page 73-74; 102pp; English.

CC The present sequence represents a human secreted polypeptide. The
 CC secreted polypeptides and polynucleotides are useful for treating
 CC nervous and muscular diseases, for inhibiting tumour formation and
 CC metastasis, for treating gastrointestinal ulceration, for preventing
 CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,
 CC renal gland, small intestine, heart, trachea, thymus, lymph node,
 CC muscular system and colon, for treating lipase deficiency in cystic
 CC fibrosis and pancreatitis, for treating undesirable clot formation
 CC such as myocardial infarction, during angioplasty and all surgical
 CC procedures that require decreased blood clot formation, for treating
 CC liver diseases, coagulation disorders and microbial diseases, for
 CC treating immune disorders, for treating inflammation and transplant
 CC rejection, for enhancing bone thickness and increasing bone density,
 CC for reducing the loss of essential ferrooxidases, for suppressing
 CC apoptosis, and for regulating vascular smooth cell proliferation. They
 CC may also be used as vaccines.

CC Sequence 255 AA;

CC Query Match 28.5%; Score 885; DB 22; Length 255;

CC Best Local Similarity 37.8%; Pred. No. 1.2e-53;

CC Matches 196; Conservative 5; Mismatches 30; Indels 288; Gaps 7;

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QY 60 NTVGEMPMQASVTRQGAHICGSLVADTWVLTAAHCFEAAATELMSWSVGLSLOREG 119
    |||||
Db 6 NAOPGTWPMQVSLHHGGHICGSLIAPSWLSAHCFTMG-----ROY 49
QY 120 LSPGAEVGVAAALP-----RAYNHSQSGDLALLQAHPTTPTCLPPARFPFGA 174
    |||||
Db 50 RCPETRRTRSA---LPRKRRRAVNHYSQSGDLALLQAHPTTPTCLPPARFPFGA 106
QY 175 SCWATGMDQDTS-----APGTLRNLRRLISRPTNCIYNQHLHNSPARPGMLCG 228
    |||||
Db 107 SCWATGMDQDTSAPSLSPAGCTLRNLRRLISRPTNCIYNQHLHNSPARPGMLCG 166
QY 229 GPOGVGPGCGDGGSPVLCLEPDGHWVQAGIISFASCAQEDAPVLLTNTAAHSMWLOA 288
    |||||
Db 167 GPOGVGPGCG----- 177
QY 289 RVQGAFLAQSPTPEMSDESDCVACSLRTAGPQAGAPSPWPWEARLMHQGLACGAL 348
    |||||
Db 178 ----- 177
QY 349 VSEAVLTAHCFIGRQAPPEWSVGLGTRPEEMGLKOLIHGAYTHPEGYDMALLLQAQ 408
    |||||
Db 178 ----- 177
QY 409 PVTLGASLRPLCLPYPDHHLDPGERGWLGRARPAGAGISLOTVPVTLGPRACSLHAA 468
    |||||
Db 178 ----- 177
QY 469 PGDGSPIPLPGWCTSAVAGELPSCGSLGAPLVHEVRGTWFLAGHSFGDACQGPAPPAV 528
    |||||
Db 178 ----- 212
QY 529 FTALPAYEDWVSSLDW--QVYFAEPPEPEAPGSCLANIS 565
    |||||
Db 213 FTALPAYE--TGSVAVTRQVYFAEPPEPEAPGSCLANIS 249

```

Search completed: January 6, 2004, 10:01:15
 Job time : 49 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2004, 09:55:46 ; Search time 17 Seconds
(without alignments)
1579.544 Million cell updates/sec

Title: US-09-978-194a-132

Perfect score: 3108
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	449	14.4	290	1 MPN_HUMAN	Q9bfr3 homo sapien
2	437.5	14.1	343	1 PSS8_HUMAN	Q16651 homo sapien
3	422	13.6	342	1 PSS8_RAT	Q9e8r7 rattus norv
4	417	13.4	306	1 BSS4_MOUSE	Q9e8r10 mus musculu
5	414	13.3	342	1 PSS8_MOUSE	Q9e8d1 mus musculu
6	400	12.9	317	1 BSS4_HUMAN	Q9e8n4 homo sapien
7	382	12.3	321	1 TRYG_HUMAN	Q9ntr2 homo sapien
8	371.5	12.0	812	1 PLMN_MOUSE	P20918 mus musculu
9	370.5	11.9	790	1 PLMN_PIG	P06867 sus scrofa
10	368.5	11.9	324	1 TEST_MOUSE	Q9j1j7 mus musculu
11	368.5	11.9	855	1 ST14_MOUSE	P56677 mus musculu
12	363	11.7	311	1 TRYG_MOUSE	Q9eql7 mus musculu
13	361.5	11.6	855	1 ST14_HUMAN	Q9j5y6 homo sapien
14	359.5	11.6	810	1 PLMN_HUMAN	P00747 homo sapien
15	359	11.6	454	1 TM53_HUMAN	P57727 homo sapien
16	359	11.6	810	1 PLMN_ERIEU	Q29485 extiracous e
17	356.5	11.5	457	1 TM53_HUMAN	Q9h3s3 homo sapien
18	356.5	11.5	812	1 PLMN_BOVIN	P06868 bos tauris
19	355.5	11.4	338	1 PLMN_HORSE	P80010 equus caball
20	354	11.4	422	1 DES1_HUMAN	Q9u152 homo sapien
21	353.5	11.4	333	1 PLMN_CANFA	P80009 canis fam11
22	353	11.4	417	1 HEP8_HUMAN	P05981 homo sapien
23	351.5	11.3	810	1 PLMN_MACMU	P12545 macaca mula
24	348.5	11.2	453	1 TM53_MOUSE	Q9e8t0 mus musculu
25	347.5	11.2	455	1 TM52_MOUSE	Q9e8t4 mus musculu
26	345.5	11.1	490	1 TM52_MOUSE	Q9j1q8 mus musculu
27	344	11.1	314	1 TEST_HUMAN	Q9y6m0 homo sapien
28	342	11.0	4548	1 APOA_HUMAN	P08619 homo sapien
29	339	10.9	1420	1 APOA_MACMU	P14417 macaca mula
30	338	10.9	343	1 PLMN_SHEEP	P81286 ovis aries
31	337.5	10.9	638	1 KAL_HUMAN	P03952 homo sapien
32	336	10.8	270	1 TRY1_MERUN	P50342 meriones un
33	335	10.8	275	1 TRY1_CANFA	P15944 canis fam11

34	335	10.8	436	1 HEP8_MOUSE	O35453 mus musculu
35	333	10.7	276	1 MCT6_MOUSE	P21845 mus musculu
36	330.5	10.6	273	1 MCT7_MOUSE	Q02844 mus musculu
37	330	10.6	271	1 EL2_MOUSE	P05208 mus musculu
38	330	10.6	275	1 TRY1_PIG	Q9n2d1 sus scrofa
39	329	10.6	275	1 TRB1_HUMAN	O15661 homo sapien
40	329	10.6	275	1 TRB2_HUMAN	P20231 homo sapien
41	329	10.6	492	1 TM52_HUMAN	O15393 homo sapien
42	328.5	10.6	274	1 MCT6_RAT	P50343 rattus norv
43	326.5	10.5	418	1 HATT_HUMAN	O60235 homo sapien
44	326.5	10.5	625	1 FAL1_HUMAN	P03951 homo sapien
45	326.5	10.5	638	1 KAL_MOUSE	P26262 mus musculu

ALIGNMENTS

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RESULT 1
MPN_HUMAN
ID MPN_HUMAN STANDARD; PRT; 290 AA.
AC Q9BFR3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Marapsin precursor (EC 3.4.21.-).
GN MPN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Fortunato M., Dando P.M., Rawlings N.D., Barrett A.J.;
RT "Cloning, sequencing and expression of marapsin, a human serine
RT proteinase.",
RL Submitted (MAR-2001) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC
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CC -----
DR EMBL: AJ306593; CAC35467.1; -.
DR HSSP: P00734; IUVS.
DR MEROPS: S01.074; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser. protease_Try.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRY_PSP_1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Zymogen; Signal; Glycoprotein.
FT SIGNAL 1 22
FT PROPEP 23 34
FT CHAIN 35 290
FT DOMAIN 35 277
FT ACT_SITE 75 75
FT ACT_SITE 124 124
FT ACT_SITE 229 229
FT DISULFID 60 76
FT DISULFID 158 235
FT DISULFID 191 214
FT DISULFID 225 253
FT CARBOHYD 55 55
FT CARBOHYD 79 79
SQ SEQUENCE 290 AA; 31940 MW; 67BDC33ECT0BFF7B CRC64;

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Db 155 LPAANASPNGLHCTVTGKHVAPSVSLTPKPLQOLEVPLSRETCLNYIDAKPEEP 214
QY 219 NPARBMLCGQPGQPOVQPGCGDGGSPVLCLEPDGHVWVQAGIISPASSCAQEDAPVLLTN 278
Db 215 HFVQEDWVCAGVVEGGKACCGDSGGLSC-PVEGLMYLTGLVSGDAGCANRRGVYTL 273
QY 279 TRAHSSWILQARV---GGAFLAQSPTETPMSEDSQVACGS-----LR----- 318
Db 274 ASSVASWISQSKYTELOPRV---POTOE-SQPSDNL-CGSHLAFSSAPAQGLRLPILFL 327
QY 319 TAGPQAGAPSPW 330
Db 328 PLGLALGLLSPW 339

RESULT 3
PSS8 RAT STANDARD; PRT; 342 AA.
ID PSS8 RAT STANDARD; PRT; 342 AA.
AC Q9ES87; Q9ER01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Proctasin precursor (EC 3.4.21.-).
GN PRS58.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Adachi M., Kitamura K., Miyoshi T., Tomita K.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Wang C.;
RL "Molecular cloning and expression of rat proctasin.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT AND HEAVY, HELD BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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CC EMBL; AB017638; BAB20281.1; -
CC EMBL; AF202076; AAG32641.1; -
CC HSSP; P00734; IUVS.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_fry.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SMART0222; CHYMOTRYPSIN.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Serine protease; Zymogen; Signal; Glycoprotein; Transmembrane.
FT SIGNAL 1 29
FT PROPEP 30 32 POTENTIAL.
FT CHAIN 33 44 PROCTASIN LIGHT CHAIN.
FT CHAIN 45 322 PROCTASIN HEAVY CHAIN.
FT PROPEP 323 342 BY SIMILARITY.

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FT TRANSMEM 320 340 POTENTIAL.
FT DOMAIN 45 286 SERINE PROTEASE.
FT DISULFID 37 154 INTERCHAIN (BY SIMILARITY).
FT DISULFID 70 86 BY SIMILARITY.
FT DISULFID 168 244 BY SIMILARITY.
FT DISULFID 201 223 BY SIMILARITY.
FT DISULFID 234 262 BY SIMILARITY.
FT ACT_SITE 85 85 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 134 134 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 17 17 I -> V (IN REF. 1).
FT CONFLICT 292 292 A -> V (IN REF. 1).
SQ SEQUENCE 342 AA; 36843 MW; 5ED1AF05D9213B98 CRC64;

Query Match 13.6%; Score 422; DB 1; Length 342;
Best Local Similarity 36.2%; Pred. No. 3.4e-21;
Matches 93; Conservative 41; Mismatches 105; Indels 18; Gaps 6;

QY 59 GNTVGEPMQASVRRQGAHICGSLVADTWLTPAHCFEKAATELMSWSVIGSLQRE 118
Db 49 GSAKPGQMPQOVSIYNGVHVCGLSVGNQWVSAHCFPREHSKE--EYEVKGAHQLD 106
QY 119 GLSPAEVEGVAAQLPRAVYHYHSGSDLLQLAHPTRHT---PLCLPQPARHPPGGA 174
Db 107 SFSNDIVVHTVAQIISHSYREBSQGDIALIRLSSPVTFRYIRPDLPAANASFPNGL 166
QY 175 SCWATG----DQTSAPGTLRNLRRLISRPNCINCYQLHQRHLNPARPGMLCGSP 230
Db 167 HCTVTGKHVAPSVSLQTPRPQOLEVPLISRETSCLYINNAVDEEHTITQDMWLCAGY 226
QY 231 QPGVQPGCGDGGSPVLCLEPDGHVWVQAGIISPASSCAQEDAPVLLTNAAHSSWILQ--- 287
Db 227 VKGGRDACCQSGSGGLSC-PIDGLVLYLGLVSWGDACAPRPGVYTLTSTYASVTHHHV 285
QY 288 ARVGAALFLAQSPTETPE 304
Db 286 AELQPRAV-----POTOE 298

RESULT 4
BS54_MOUSE STANDARD; PRT; 306 AA.
ID BS54_MOUSE STANDARD; PRT; 306 AA.
AC Q9ER10;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
GN Brain-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mitani S., Okui A., Kominami K., Yamaguchi N.;
RL "Cloning and characterization of a novel serine protease, mBSSP-4.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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CC EMBL; AB010778; BAB20262.1; -
CC HSSP; P00763; IDPO.
DR MEROPS; S01.252; -
DR MGI; MGI:191805; 4733401N09R1k.

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DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin.1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYPSIN_DOM.1.
 DR PROSITE: PS00240; TRYPSIN_DOM.1.
 DR PROSITE: PS00134; TRYPSIN_HIS.1.
 DR PROSITE: PS00135; TRYPSIN_SER.1.
 DR HydroLase; Serine protease; signal.
 KW SIGNAL 1 32
 FT CHAIN 33 306 BRAIN-SPECIFIC SERINE PROTEASE 4.
 FT ACT_SITE 90 90 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 141 141 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 242 242 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 75 91 BY SIMILARITY.
 FT DISULFID 175 248 BY SIMILARITY.
 FT DISULFID 208 227 BY SIMILARITY.
 FT DISULFID 238 266 BY SIMILARITY.
 FT CARBOHYD 70 70 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 306 AA; 33262 MW; FBBF03C0C285E7E8 CRC64;

Query Match 13.4%; Score 417; DB 1; Length 306;
 Best Local Similarity 33.7%; Pred. No. 6.5e-21;
 Matches 106; Conservative 55; Mismatches 114; Indels 40; Gaps 13;

QY 8 SLAGSVYLLMILFEVLYDFCIYVAINVSLMISFRKVOEPQKARHGNVTPE-- 65
 DB 9 ALGGDPFSLILLLVL-----TSYAPISAAT-----RVSPDCGKPOQLNRIVGEGDS 56
 QY 66 -----NFWQASVRRQGNHICSGSLVADTWVLTAAHCEKAATELNSWSVYLSGLOREGIS 121
 DB 57 MDAQWMIWISILNKGSHHCAGSLITRWVWYTAHCF-KSNMDKPSLFSVLLGKMGKLSFG 115
 QY 122 PGAEVGVALLQPRAYNHYSG--SDALLQLAHPHTHT---PLCLPQAPHRFPFGAS 175
 DB 116 PISQKGIAMV-LPHRYGKMECTHADIALVRLHEHIOFSERLPLCLPDSVRLPKTD 174
 QY 176 CWATGW----DQTSAPGTLRLRLISPTCNCIYNQLHQRHLSNPA-RPGMLCGSP 230
 DB 175 CWIAGWSIODGVPRLPHQTLQKLKVIIDSELCKSLY---WRGAGQAPATEGMKLCAGY 230
 QY 231 QGVGPGCGGSGGVLCLPDPGHVQAGISFASCAQEDAPVLLTNTAAHSMVQARV 290
 DB 231 LGEGRDACCSDSGGSLMCG-QVDDHWLLTGLISWEGCA-DDRGVYVTLAHSWQRTIV 288
 QY 291 QGA---AFLAOSPET 302
 DB 289 QGVQLRGVLAIDSGDT 303

RESULT 5
 PSS8 MOUSE STANDARD; PRT; 342 AA.
 AC 09ESTL,
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Prostatein precursor (EC 3.4.21.-) (Channel activating protease 1).
 GN PSS8 OR CAPI.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20235202; PubMed=10770960;
 RA Vaugeois G., Vallet V., Jaeger N.F., Pfister C., Bens M., Farman N.,
 RA Coutais-Couty N., Vandewalle A., Rossier B.C., Hummler E.,
 RT "Activation of the amiloride-sensitive epithelial sodium channel by
 the serine protease mCAP1 expressed in a mouse cortical collecting
 duct cell line."
 RL J. Am. Soc. Nephrol. 11:828-834(2000).
 CC -!- FUNCTION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY (BY

CC SIMILARITY). ACTIVATES AMILORIDE-SENSITIVE SODIUM CHANNELS.
 CC -!- SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT AND HEAVY, HELD BY A
 CC DISULFIDE BOND (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF
 CC ITS C-TERMINUS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
 CC FRAMESHIFT IN POSITION 339.
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 CC -----
 DR EMBL: AF188613; AAC17054.1; ALT_FRAME.
 DR HSSP: P00734; IUVS.
 DR MEROPS: S01.158; -.
 DR MGD: MG1.1923810; PSS8.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin.1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYPSIN_DOM.1.
 DR PROSITE: PS00240; TRYPSIN_DOM.1.
 DR PROSITE: PS00134; TRYPSIN_HIS.1.
 DR PROSITE: PS00135; TRYPSIN_SER.1.
 KW HydroLase; Serine protease; Zymogen; signal; Glycoprotein;
 KM Transmembrane.
 FT SIGNAL 1 29
 FT PROPEP 30 32 POTENTIAL.
 FT CHAIN 33 342 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 45 322 PROSTATIN LIGHT CHAIN.
 FT PROPEP 323 342 PROSTATIN HEAVY CHAIN.
 FT TRANSMEM 320 340 BY SIMILARITY.
 FT DOMAIN 45 286 POTENTIAL.
 FT DISULFID 37 154 SERINE PROTEASE.
 FT DISULFID 70 86 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 168 244 BY SIMILARITY.
 FT DISULFID 201 223 BY SIMILARITY.
 FT DISULFID 234 262 BY SIMILARITY.
 FT ACT_SITE 85 85 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 134 134 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 110 110 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 342 AA; 36729 MW; 0620DE88ED187D0F CRC64;

Query Match 13.3%; Score 414; DB 1; Length 342;
 Best Local Similarity 35.2%; Pred. No. 1.2e-20;
 Matches 92; Conservative 41; Mismatches 102; Indels 26; Gaps 6;

QY 59 GNTVPEMPQASVRRQGNHICSGSLVADTWVLTAAHCEKAATELNSWSVYLSGLORE 118
 DB 49 GSAKGGQMPWQVSYITDGNHVCGSLVSNKMWVSAHCFPREHSRE--AYEVKGAHQD 106
 QY 119 GLSPGAEEVGVALLQPRAYNHYSGSDALLQLAHPHTHT---PLCLPQAPHRFPFGA 174
 DB 107 SYSNDTVVHTVAQIITHTSSYREBSGQGIARFLRSLPFTFSYIRPICLPANASFPWGL 166
 QY 175 SCWATGW----DQTSAPGTLRLRLISPTCNCIYNQLHQRHLSNPARPGMLCGSP 230
 DB 167 HCTVTKGKHVAPSVLQTPRLPQLQLEVLISGETSCLYINAVPEEHTTIOQDMLCAGY 226
 QY 231 QGVGPGCGGSGGVLCLPDPGHVQAGISFASCAQEDAPVLLTNTAAHSMV----- 285
 DB 227 VVGKGDACCQDGGGGLSC-PMEGIWYLAGIVSWDCAQAPNRPVYVTLTSTVASIHHIV 285
 QY 286 --LQARVQGAFLAOSPETPE 304
 DB 286 AELQPRV-----VPQTE 298

RESULT 6
 BSS4_HUMAN STANDARD; PRT; 317 AA.
 AC O9GN4; O43342; (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Brain-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4)
 DE (SP0011A)
 GN PRS822 OR PRS826 OR BSSP4.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Mitsui S., Okui A., Kominami K., Yamaguchi N.;
 RT "Cloning and characterization of a human brain-specific serine
 RT protease, hBSSP-4.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=pancreas;
 RA Wong G.W., Stevens R.L.;
 RT "Identification of a new member of the chromosome 16 family of serine
 RT proteases.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=pancreas;
 RA MEDLINE=2238257; PubMed=12477932;
 RA Strusberg R.L., Felting E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D.,
 RA Allschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stancovski M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brakenstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
 RA Rahn S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., Moban P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kertman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 47-317 FROM N.A.
 RA Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunders E.,
 RA Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S.,
 RA Goodwin L., Bryant J., Teemer J., Meincke L., Longmire J., White S.,
 RA Ueng S., Tatum O., Campbell C., Fawcett J., Deaven L.,
 RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RL -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 11.
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 CC EMBL; AB010779; BAB20263.1; -
 DR EMBL; AF321182; AAG35070.1; -

DR EMBL; BC009726; AA09726.1; -
 DR EMBL; AC003965; AAB93671.1; -
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01.252; -
 DR Genew; HGNC:14368; PRS822.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR KMW; Hydrolyase; Serine protease; Signal.
 FT SIGNAL 1 32
 FT CHAIN 33 317
 FT ACT_SITE 90 90
 FT ACT_SITE 141 141
 FT ACT_SITE 242 242
 FT DISULFID 75 91
 FT DISULFID 175 248
 FT DISULFID 208 227
 FT DISULFID 238 266
 FT CARBOHYD 70 70
 FT CONFLICT 47 47
 SQ SEQUENCE 317 AA; 33731 MW; E2A123B86E79935 CRC64;
 Query Match 12.9%; Score 400; DB 1; Length 317;
 Best Local Similarity 30.8%; Pred. No. 9.1e-20;
 Matches 99; Conservative 57; Mismatches 123; Indels 42; Gaps 11;
 QY 27 CIVCTITVAIVNSLMTLSFRVQEPQ--GKAKRHGNTVPG-----EMPQASVRRQGAH 78
 DB 14 CIGRTFSLLLASTAIVLMAARIPVPACQKPOQLNRVVVGSDSTSEMPVITSIGKGNH 73
 QY 79 ICSSGLVADTVLTLAHCPEKAATELNS---WSYVLGSLQREGISPAEVEYVALQLP 135
 DB 74 HCAGSLILSRVWITAAHCFK----DNLKPYLPSVLGAMQJLGNRSGRSQKGVAMVE-P 128
 QY 136 RAYNHYSG--SPALLLAPHTHT-----PLCLPQPHRPFPGASCWATGW---PDQT 185
 DB 129 HPVYSWKEGACADIVLWERSIQSERVLPICLPDAIHLHPNTHCISGWSIQDQVP 188
 QY 186 SDAPETLNLRLRLSRPTCNQIYQLHQRHLSNPARGMTCGPGQPGVQCGDSCGP 245
 DB 189 LPHPTLKLKXVPIIDSEVCHLY---WRGAGQGITEDMCLAGYLBEBRDACLDSCGP 245
 QY 246 VLCEPDGHVQAGIISFASCAQEDAPVLLNTAAHSSWLOARVQGAAPLAQSPETPEM 305
 DB 246 LMC-QVDGAWMLAGIISWEGCAERNRPGVYISLSAHSRWEKIVQGVQLRGAQ----- 299
 QY 306 SDEDSVACGSLRTAGPQGA 326
 DB 300 -----GGALRAPSGSGA 313
 RESULT 7
 TRYX_HUMAN STANDARD; PRT; 321 AA.
 AC O9NRR2; O9C015; O9NR08; O9UBB2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
 GN TP8G1 OR TMT.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2).
 RX MEDLINE=20302813; PubMed=10843716;
 RA Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallao M.,

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." J.
RL Proc. Natl. Acad. Sci. U.S.A. 99:16689-16903(2002).
[4]
RN SEQUENCE OF 1-16 FROM N.A.
RP STRAIN=129/SVJ; TISSUE=Liver;
RX PubMed=12149246;
RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
RA Farmer R.J., Miles L.A.;
RT "Localisation of regulatory elements mediating constitutive and
RT cytokine-stimulated plasminogen gene expression." J.
RL J. Biol. Chem. 277:38579-38588(2002).
[5]
RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RP MEDLINE=95042728; PubMed=7525077;
O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma." J.
RL Cell 79:315-328(1994).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAFIAAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLEGENASE AND SEVERAL COMPLEMENT ZYMOSINS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
CC NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
CC METASTATIC TUMORS IN VIVO.
CC -1- CATALYTIC ACTIVITY: preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
CC INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD
CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 5 kringie domains.
CC -----
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CC -----
DR EMBL: J04766; AAA50168.1; -;
DR EMBL: AF481053; AAM22156.1; -;
DR EMBL: BC014773; AAH14773.1; -;
DR EMBL: AY134430; AAN15805.1; -;
DR PIR: A38514; PLMS.
DR HSSP: P00747; 1PMK.
DR MEROPS: S01.233; -;
DR MGD: MGI.97620; P1g.
DR GO: GO:0016506; F:apoptosis activator activity; IDA.
DR GO: GO:0006915; P:apoptosis; IDA.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringie.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00051; kringie; 5.

DR Pfam: PF00024; PAN. 1.
DR Pfam: PF00089; trypsin. 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR PRODOM: PD000395; Kringie; 5.
DR SMART: SM00130; KR; 5.
DR SMART: SM00473; PAN AP; 1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00021; KRINGLE 1; 5.
DR PROSITE: PS50070; KRINGLE 2; 5.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydroxylase, Serine protease; Plasma; Glycoprotein; fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringie; Zymogen; Repeat;
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 812 PLASMINOGEN.
FT CHAIN 20 581 PLASMIN HEAVY CHAIN A.
FT PEPTIDE 20 97 ACTIVATION PEPTIDE.
FT CHAIN 98 581 PLASMIN SHORT FORM OF CHAIN A.
FT CHAIN 98 2436 ANGIOSTATIN.
FT CHAIN 582 812 PLASMIN LIGHT CHAIN B.
FT DOMAIN 103 181 KRINGLE 1.
FT DOMAIN 184 262 KRINGLE 2.
FT DOMAIN 275 352 KRINGLE 3.
FT DOMAIN 377 454 KRINGLE 4.
FT DOMAIN 481 560 KRINGLE 5.
FT DOMAIN 582 812 SERINE PROTEASE.
FT ACT_SITE 624 624 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 667 667 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 762 762 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 49 73 BY SIMILARITY.
FT DISULFID 53 61 BY SIMILARITY.
FT DISULFID 103 181 BY SIMILARITY.
FT DISULFID 124 164 BY SIMILARITY.
FT DISULFID 152 176 BY SIMILARITY.
FT DISULFID 185 262 BY SIMILARITY.
FT DISULFID 188 316 BY SIMILARITY.
FT DISULFID 206 245 BY SIMILARITY.
FT DISULFID 234 257 BY SIMILARITY.
FT DISULFID 275 352 BY SIMILARITY.
FT DISULFID 296 335 BY SIMILARITY.
FT DISULFID 324 347 BY SIMILARITY.
FT DISULFID 377 454 BY SIMILARITY.
FT DISULFID 398 437 BY SIMILARITY.
FT DISULFID 426 449 BY SIMILARITY.
FT DISULFID 481 560 BY SIMILARITY.
FT DISULFID 502 543 BY SIMILARITY.
FT DISULFID 531 555 BY SIMILARITY.
FT DISULFID 568 687 INTERCHAIN (BY SIMILARITY).
FT DISULFID 578 586 INTERCHAIN (BY SIMILARITY).
FT DISULFID 609 625 BY SIMILARITY.
FT DISULFID 701 768 BY SIMILARITY.
FT DISULFID 731 747 BY SIMILARITY.
FT DISULFID 758 786 BY SIMILARITY.
FT CONFLICT 235 235 R -> H (IN REF. 1).
FT CONFLICT 525 525 G -> D (IN REF. 1).
FT CONFLICT 649 649 S -> L (IN REF. 1).
SQ SEQUENCE 812 AA; 90781 MW; 241732608A2FFD2 CRC64;
Query Match 12.0%; Score 371.5; DB 1; Length 812;
Best Local Similarity 32.7%; Pred. No. 2e-17;
Matches 93; Conservative 45; Mismatches 107; Indels 39; Gaps 11;
QY 23 LYDPCIVCTTYAVINVSIMWLSFRKVOEPOGKAR-HGNTV-----PGEWPMQASVRRQ 75
DB 551 LYDYCDIPLGASA-----SFECKGQYEPKCKPCRRVVGCVANPHSWPMQISLRR 602
QY 76 --GAHICGSLVADWTUTLAHCEKAATLNSWSVLSGLQREGSLSPAGEEYVALQ 133
DB 603 FTGQHFCCGTLIADBEWVLTAAHCEKSSRPEF--YKVLGAHEEYIRGSDVOEISVAKLI 660

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Testis precursor (EC 3.4.21.-) (Trypsin 4).
 GN PRSS21.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv.
 RX MEDLINE=21153229; PubMed=11231276;
 RA Scarmen A.L., Hooper J.D., Boucaut K.J., Sit M.-L., Webb G.C.,
 RA Norwylle J.F., Antalis T.M.,
 RT "Organization and chromosomal localization of the murine Testis gene
 RT encoding a serine protease temporally expressed during
 RT spermatogenesis.";
 RL Eur. J. Biochem. 268:1250-1258(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAUB/C; TISSUE=Testis;
 RX PubMed=11259427;
 RA Wong G.W., Li L., Madhusudan M.S., Krilis S.A., Gurish M.F.,
 RA Rothenberg M.E., Sali A., Stevens R.L.,
 RT "Trypsin 4, a new member of the chromosome 17 family of mouse serine
 RT proteases.";
 RL J. Biol. Chem. 276:20648-20658(2001).
 RN [3]
 RP SEQUENCE OF 3-324 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Aachi S., Fukuda S.,
 RA Katada K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochua H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okada T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: COULD REGULATE PROTEOLYTIC EVENTS ASSOCIATED WITH
 CC TESTICULAR GERM CELL MATURATION.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 CC (Potential).
 CC -1- TISSUE SPECIFICITY: Testis.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN POST-MEIOTIC TESTICULAR GERM
 CC CELLS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1
 CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A STOP
 CC CODON IN POSITION 315.
 CC -----
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 CC -----
 CC EMBL; AF304012; AAK293360.1; -
 CC EMBL; AY005145; AAG02255.1; -
 CC EMBL; AF176209; AAF64407.2; -

DR EMBL; AF226710; AAF64428.2; -
 DR EMBL; AK006271; -; NOT_ANNOTATED_CDS.
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01.011; -.
 DR MGD; MGI:191698; Prss21.
 DR GO; GO:0005624; C:membrane fraction; IDA.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00089; trypsin.1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYPSIN_DOM.1.
 DR PROSITE; PS00240; TRYPSIN_DOM.1.
 DR PROSITE; PS00134; TRYPSIN_HIS.1.
 DR PROSITE; PS00135; TRYPSIN_SER.1.
 DR HydroLase; Serine protease; Glycoprotein; Signal; GPI-anchor; Zymogen.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 54 POTENTIAL.
 FT CHAIN 55 298 TESTISIN.
 FT PROPEP 299 324 REMOVED IN MATURE FORM (POTENTIAL).
 FT ACT_SITE 95 95 CHARGE RELAY SYSTEM (POTENTIAL).
 FT ACT_SITE 147 147 CHARGE RELAY SYSTEM (POTENTIAL).
 FT ACT_SITE 248 248 CHARGE RELAY SYSTEM (POTENTIAL).
 FT DISULFID 46 167 POTENTIAL.
 FT DISULFID 80 96 POTENTIAL.
 FT DISULFID 181 254 POTENTIAL.
 FT DISULFID 214 233 POTENTIAL.
 FT DISULFID 244 272 POTENTIAL.
 FT LIPID 298 298 GPI-ANCHOR (POTENTIAL).
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 275 275 P -> H (IN REF. 3).
 SQ SEQUENCE 324 AA; 36175 MW; 56DC59E84F3C3CD4 CRC64;

Query Match 11.9%; Score 368.5; DB 1; Length 324;
 Best Local Similarity 29.2%; Pred. No. 1.1e-17;
 Matches 88; Conservative 56; Mismatches 122; Indels 35; Gaps 10;

QY 28 IVCTTVAIVNSLWMLSF---RVQEPQKAKRHGN-TVP-----GEMPMQAS 71
 DB 12 LVVAITAMALQSYLYLOVDPKPELPDLISGCGHHTTSRVIGGDDELGLGPMQGS 71
 QY 72 VRROGAHICSGSLADVTWLTALACFEKAATELNSWVLSQRE---GLSPGAEV 127
 DB 72 LRWGNHICGATLNRNWLTAHCFOK--DNDFPDWTVOGELTSRPSLWNLQAYSRY 129
 QY 128 GVAALQIPRAYNHYSQGSDDLALQLAHPTHT---PLCLPQPAHREPPGASCWATGW-- 181
 DB 130 QIEDIFLSPKYSF-QYPNDIALKLSSPVTYNNFIPLCLNSTYKFENRTDCWWTGWA 188
 QY 182 --DDTSDAPGTLNLRRLISRPTCNCINYQLHQRHLSNAPRGMLCGSPQVQGPCQ 239
 DB 189 IGEDESLESPNTLOEVQVAIINNSCMHYKKPDR--TNWGDWVCAGPEGGKACF 245
 QY 240 GDSCGPVLCLEPPDGHVQAGIISPASSQAOEDAVLLTNTAHSWLOARVQGAFLAQS 299
 DB 246 GDSCGPVLCLEPPDGHVQAGIISPASSQAOEDAVLLTNTAHSWLOARVQGAFLAQS 304
 QY 300 P 300
 DB 305 P 305
 RESULT 11
 ID ST14_MOUSE STANDARD; PRT; 855 AA.
 AC P56677;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Epithin).
 GN ST14 OR PRSS14.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C.B.17SC1D; TISSUE=Thymus;
 RC MEDLINE=99216440; PubMed=1019918;
 RA Kim M.G., Chen C., Lyu M.S., Cho E.G., Park D., Kozak C.,
 RA Schwartz R.H.;
 RT "Cloning and chromosomal mapping of a gene isolated from thymic
 RT stromal cells encoding a new mouse type II membrane serine protease,
 RT epithin, containing four LDL receptor modules and two CUB domains.";
 RL Immunogenetics 49:420-428(1999).
 RN [2]
 RP REVISIONS TO 23; 321; 325; 343; 409-410 AND C-TERMINUS.
 RC STRAIN=C.B.17SC1D; TISSUE=Thymus;
 RA Kim M.G., Chen C., Cho E.G., Park D., Schwartz R.H.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stalder M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bosak S.A., Loquellano N.A., Peters G.J., Abramson R.D., Walling S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smolius D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marx M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN INTESTINE, KIDNEY, LUNG,
 CC AND THYMUS. NOT EXPRESSED IN SKELETAL MUSCLE, LIVER, HEART,
 CC TESTIS, AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: Contains 4 LDL-receptor class A domains.
 CC -1- SIMILARITY: Contains 2 CUB domains.
 CC -----
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 CC -----
 CC EMBL; AF042822; AAD02230.3; -;
 DR EMBL; BC005496; AAH05496.1; -;
 DR HSSP; P20231; JAO.
 DR MEROPS; S01.302; -;
 DR MGD; MGI:133881; St14.
 DR GO; GO:0005576; C:extracellular; IDA.
 DR GO; GO:0019897; C:extrinsic to plasma membrane; IDA.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000859; CUB domain.
 DR InterPro; IPR002172; LDL_receptor_A.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00057; Idl_recept_a; 4.
 DR Pfam; PF00089; trypsins; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00261; LDLRECEPTOR.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00192; LDLa; 4.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01209; LDLa_1; 2.
 DR PROSITE; PS00068; LDLa_2; 4.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Signal anchor; Glycoprotein; Hydrolase; Serine protease;
 KW Transmembrane; Repeat.
 FT DOMAIN 1
 FT TRANSMEM 56 76
 FT FT 55
 FT FT 76
 FT DOMAIN 77 955
 FT FT 214 331
 FT DOMAIN 340 444
 FT DOMAIN 451 488
 FT DOMAIN 489 522
 FT DOMAIN 523 561
 FT DOMAIN 565 604
 FT DOMAIN 615 854
 FT ACT_SITE 656 656
 FT ACT_SITE 711 711
 FT ACT_SITE 805 805
 FT CARBOHYD 107 107
 FT CARBOHYD 302 302
 FT CARBOHYD 365 365
 FT CARBOHYD 421 421
 FT CARBOHYD 489 489
 FT CARBOHYD 772 772
 SQ SEQUENCE 855 AA; 94654 MW; 4F10B84DA2146D5 CRC64;

Query Match 11.9%; Score 368.5; DB 1; Length 855;
 Best Local Similarity 32.8%; Pred. No. 3.3e-17;
 Matches 85; Conservative 38; Mismatches 105; Indels 31; Gaps 8;

QY 44 SPRKQEPQGRKAKRGNTVPGEPMQASVRQG-AHICSGSLVATQWTLAHCFE---X 99
 DB 608 SFTK---QARVGGTNDDEGEPMQVSHALGCHGLCASLISDWLSAAHCHQDDKN 663
 QY 100 AATELNSMSVVLGSLQEGSLPGAEVVALQLPR-----AVNHYSGSDLLALQL-- 152
 DB 664 FKYSYTWMTATFLGLDLSKXSAS---GVGLKAKRIITHSFNDFPFYDIALLELEK 719
 QY 153 --AHPTHTPLCLPQPAHPPFGASCWATGWDQDTSAPGT--LNLRLRLISPTCNCI 208
 DB 720 SVEYSTVVRPFLCPATHVFPAGKAIWVGHTKGGTGALILQKEIRVINQTTCEDL 779
 QY 209 YNQLHQRHLSNARPGMCGGPPQGVQPCQDSCGPPVLCLEPPDHVQAGISFASSCA 268
 DB 780 MFO-----QITRMKCVGLSGVDSCQDSSGPPSSAKEDRMFQAGVSWEGCA 831
 QY 269 CEDAPVLTLNTPAHSMLQ 287
 DB 832 QNKGCVTRLPVARDWIK 850

RESULT 12
 TRYG MOUSE STANDARD; PRT: 311 AA.
 ID ID TRYG MOUSE
 AC 09OUI7;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Trypsase Gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
 GN TPSC1 OR TMT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxId=10090;

RT of human plasminogen and their interaction with the NH₂-terminal
RT activation peptide as studied by affinity chromatography."
RL Eur. J. Biochem. 50:489-494(1975).
RN [6]
RP SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810.
RA Sottrup-Jensen L., Claes H., Zajdel M., Petersen T.E., Magnusson S.,
RL (in) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.),
RL Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,
RL Raven Press, New York (1978).
RN [7]
RP SEQUENCE OF 483-604.
RX MEDLINE=76043692; PubMed=126863;
RT "Wiman B., Wallen P.;
RT "Amino-acid sequence of the cyanogen-bromide fragment from human
RT plasminogen that forms the linkage between the plasmin chains."
RL Eur. J. Biochem. 58:539-547(1975).
RN [8]
RP SEQUENCE OF 581-810.
RX MEDLINE=77225245; PubMed=142009;
RA Wiman B.;
RT "Primary structure of the B-chain of human plasmin."
RL Eur. J. Biochem. 76:129-137(1977).
RN [9]
RP ACTIVE SITE.
RX MEDLINE=73149248; PubMed=4694729;
RA Robbins K.C., Bernabe P., Arzadon L., Summaria L.;
RT "The primary structure of human plasminogen. II. The histidine loop
RT of human plasmin: light (B) chain active center histidine sequence."
RL J. Biol. Chem. 248:1631-1633(1973).
RN [10]
RP ACTIVE SITE.
RX MEDLINE=69234739; PubMed=4240117;
RA Groskopf W.R., Summaria L., Robbins K.C.;
RT "Studies on the active center of human plasmin. Partial amino acid
RT sequence of a peptide containing the active center serine residue."
RL J. Biol. Chem. 244:3590-3597(1969).
RN [11]
RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RX MEDLINE=82213905; PubMed=6919539;
RA Trexler M., Vail Z., Patchy L.;
RT "Structure of the omega-aminocarboxylic acid-binding sites of human
RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
RT binding of ligand by kringles 4."
RL J. Biol. Chem. 257:7401-7406(1982).
RN [12]
RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RX MEDLINE=85054794; PubMed=6094526;
RA Vail Z., Patchy L.;
RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
RT are essential for fibrin affinity of the kringles 1 domain."
RL J. Biol. Chem. 259:13690-13694(1984).
RN [13]
RP PHOSPHORYLATION SITE SER-597.
RX MEDLINE=97345939; PubMed=9201958;
RA Wang H., Porok M., Bretthauer R.K., Castellino F.J.;
RT "Serine-578 is a major phosphorylation locus in human plasma
RT plasminogen."
RL Biochemistry 36:8100-8106(1997).
RN [14]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=88185359; PubMed=3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns."
RL Eur. J. Biochem. 173:57-63(1988).
RN [15]
RP CARBOHYDRATE-LINKAGE SITE SER-268.
RX MEDLINE=97207306; PubMed=9054441;
RA Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,
RA Pizzo S.V.;
RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of

RT human plasminogen 2."
RL J. Biol. Chem. 272:7408-7411(1997).
RN [16]
RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RX MEDLINE=95042728; PubMed=7525077;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma."
RL Cell 79:315-328(1994).
RN [17]
RP CHARACTERIZATION OF ANGIOSTATIN.
RX MEDLINE=97238710; PubMed=9102221;
RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
RA Lapcevich R., Nacy C.A.;
RT "A recombinant human angiostatin protein inhibits experimental primary
RT and metastatic cancer."
RL Cancer Res. 57:1329-1334(1997).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RX MEDLINE=92031502; PubMed=1657148;
RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
RT "Crystal and molecular structure of human plasminogen kringles 4
RT refined at 1.9-A resolution."
RL Biochemistry 30:10576-10588(1991).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RX MEDLINE=92031503; PubMed=1657149;
RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of
RT human plasminogen kringles 4."
RL Biochemistry 30:10589-10594(1991).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RA Stec B., Yamano A., Whitlow M., Teeter M.M.;
RT "Structure of human plasminogen kringles 4 at 1.68 Angstrom and 277 K.
RT A possible structural role of disordered residues."
RL Acta Crystallogr. D 53:169-178(1997).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
RX MEDLINE=96180681; PubMed=8611560;
RA Mathews I., Vanderhoff-Hanaver P., Castellino F.J., Tulinsky A.;
RT "Crystal structures of the recombinant kringles 1 domain of human
RT plasminogen in complexes with the ligands epsilon-aminocaproic acid
RT and trans-4-(aminomethyl)cyclohexane-1-carboxylic acid."
RL Biochemistry 35:2567-2576(1996).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
RX MEDLINE=98198034; PubMed=9521645;
RA Chang Y., Mochalkin I., McCance S.G., Cheng B., Tulinsky A.,
RA Castellino F.J.;
RT "Structure and ligand binding determinants of the recombinant kringles
RT 5 domain of human plasminogen."
RL Biochemistry 37:3258-3271(1998).
RN [23]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237157; PubMed=8181475;
RA Rejzante M.R., Llinas M.;
RT "1H-NMR assignments and secondary structure of human plasminogen
RT kringles 1."
RL Eur. J. Biochem. 221:927-937(1994).
RN [24]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237158; PubMed=8181476;
RA Rejzante M.R., Llinas M.;
RT "Solution structure of the epsilon-aminohexanoic acid complex of
RT human plasminogen kringles 1."
RL Eur. J. Biochem. 221:939-949(1994).
RN [25]
RP STRUCTURE BY NMR OF 183-354.
RX MEDLINE=96194156; PubMed=8652577;
RA Soehndel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
RA Rickli E.E.;

RT "Recombinant gene expression and 1H NMR characteristics of the
RT kringle (2 + 3) supermodule: spectroscopic/functional individuality
RT of plasminogen kringle domains";
RL Biochemistry 35:2357-2364(1996).
RN [26]
RP STRUCTURE BY NMR OF 374-461.
RX MEDLINE=90219023; PubMed=2157850;
RA Atkinson R.A., Williams R.J.P.,
RT "Solution structure of the kringle 4 domain from human plasminogen by
RT 1H nuclear magnetic resonance spectroscopy and distance geometry";
RL J. Mol. Biol. 212:541-552(1990).
RN [27]
RP VARIANTS PHE-374 AND THR-620.

Query Match 11.6%; Score 359.5; DB 1; Length 810;
Best Local Similarity 33.8%; Pred. No. 1.2e-16;
Matches 95; Conservative 39; Mismatches 104; Indels 43; Gaps 13;

QY 23 LVDFCIY--CITTYAINVSLMMLSPKQVPOGKAKR--HGNTY-----PGEMPMQASVR 73
DB 551 LVDYCVPOCAAP-----SF--DCGKPOVEPKKCGRVVGGCVAPHSPQVSLR 599
QY 74 -ROGAHICGSLVADTWLTAAACEKAATELINSWVLGSLQREGSLPGAEEVGAAL 132
DB 600 TRFGMFCGGTSLSPWVLTAAHCELEKSRP--SSYKVLGAHQEVNLEPHYGEIVSR 657
QY 133 QLEPRAYNYSQGSDDLALDLAHPHTHT---PICLPQAPHPFPFGASCWATGW--DQDTS 186
DB 658 FLE-----PTRKDIALKLKISPAVITDKYIPACLPSPVYVADRTCEFTIGMETQGT 711
QY 187 DAPGTARNRLRLISPTNCIYNQHLNHPARFGLCGPQGVGPGCGSGGSRV 246
DB 712 GA-GLKEAQLPTEKNVCN-----RYEFLNGRVOSTELCAGHLAGTDSQGSGBGL 764
QY 247 LCLEPDPHWQAGIISFASSCAQEDAPVLTNTAAHSMWLO 287
DB 765 VCFEKDKYILQ--GVTSWGGCARGPNKRGVYVRSRVTWIE 804

RESULT 15
TMS3 HUMAN STANDARD; PRT; 454 AA.
ID P57727;
AC TMS3 HUMAN
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transmembrane protease, serine 3 (BC 3.4.21.-) (Serine protease
DE TADG-12) (Tumor associated differentially-expressed gene-12 protein).
GN TMPRSS3 OR TADG12 OR ECHOS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A AND T).
RC TISSUE=Ovarian carcinoma.
RX MEDLINE=20521358; PubMed=11068177;
RA Underwood L.J., Shigemasa K., Tanimoto H., Beard J.B., Schneider E.N.,
RA Wang Y., Parmley T.H., O'Brien T.J.;
RT "Ovarian tumor cells express a novel multi-domain cell surface serine
RT protease";
RL Biochim. Biophys. Acta 1502:337-350(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A; B AND D), AND VARIANT ILE-53.
RX MEDLINE=20578749; PubMed=11337999;
RA Scott H.S., Kudoh J., Matenhofer M., Shibuya K., Berry A., Christ R.,
RA Guipponi M., Wang J., Kanaaki K., Asakawa S., Minoshima S.,
RA Yoniss F., Mehdi S.Q., Radhakrishna U., Pappasavas M.P., Gehrig C.,
RA Antonarakis S.E.;
RT "Insertion of beta-satellite repeats identifies a transmembrane
RT protease causing both congenital and childhood onset autosomal
RT recessive deafness";

RL Nat. Genet. 27:59-63(2001).
RN [3]
RP SUBCELLULAR LOCATION: AND FUNCTION IN ENAC CLEAVAGE.
RX PubMed=12393794;
RA Guipponi M., Vauquiaux G., Matenhofer M., Shibuya K., Vazquez M.,
RA Doucherty L., Scamuffa N., Guida E., Okui M., Rossier C., Hancock M.,
RA Bucher K., Raymond A., Hummler E., Marzella P.L., Kudoh J.,
RA Shimizu N., Scott H.S., Antonarakis S.E., Rossier B.C.;
RT "The transmembrane serine protease (TMPRSS3) mutated in deafness
RT DFNB8/10 activates the epithelial sodium channel (ENaC) in vitro";
RL Hum. Mol. Genet. 11:2829-2836(2002).
RN [4]
RP VARIANTS DFNB8/DFNB10 CYS-251 AND LEU-404.
RX MEDLINE=21354482; PubMed=11462234;
RA Masnoud S., Antonarakis S.E., Schwede T., Ghorbel A.M., Gratri M.,
RA Pappasavas M.P., Dixit M., Elgaied-Boullia A., Matenhofer M.,
RA Rossier C., Scott H.S., Ayadi H., Guipponi M.;
RT "Novel missense mutations of TMPRSS3 in two consanguineous Tunisian
RT families with non-syndromic autosomal recessive deafness";
RL Hum. Mutat. 18:101-108(2001).
RN [5]
RP VARIANTS DFNB8/DFNB10 TRP-109, PHE-194 AND ARG-407, AND VARIANTS
RP ILE-53, SER-111 AND VAL-253.
RX MEDLINE=21317610; PubMed=11424922;
RA Ben-Yosef T., Matenhofer M., Riazuddin S., Ahmed Z.M., Scott H.S.,
RA Kudoh J., Shibuya K., Antonarakis S.E., Bonne-Tamir B.,
RA Radhakrishna U., Naz S., Ahmed Z., Riazuddin S., Pandya A.,
RA Nance W.E., Wilcox E.R., Friedman T.B., Morell R.J.;
RT "Novel mutations of TMPRSS3 in four DFNB8/B10 families segregating
RT congenital autosomal recessive deafness";
RL J. Med. Genet. 38:396-400(2001).
RN [6]
RP VARIANTS DFNB8/DFNB10 GLY-103, AND VARIANTS ASN-173 AND THR-426.
RX MEDLINE=21904597; PubMed=11907649;
RA Matenhofer M., Di Iorio V., Rablone R., Dougherty L., Pampalos A.,
RA Schwede T., Montserrat-Sentis B., Arbones L., Illides T.,
RA Pasquadiibscaglia A., P'Amelio M., Alwan S., Rossier C., Dahl H.-H.M.,
RA Petersen M.B., Estivill X., Gasparini P., Scott H.S.,
RA Antonarakis S.E.;
RT "Mutations in the TMPRSS3 gene are a rare cause of childhood
RT nonsyndromic deafness in Caucasian patients";
RL J. Mol. Med. 80:124-131(2002).
RN [7]
RP FUNCTION: Probable protease. Seems to be capable of activating
RN ENaC.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
CC reticulum.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=A;
CC IsoId=p57727-1; Sequence=Displayed;
CC Name=B; Synonyms=C;
CC IsoId=p57727-2; Sequence=VSP_005391;
CC Name=D;
CC IsoId=p57727-3; Sequence=VSP_005392;
CC Name=E; Synonyms=Truncated, TADG-12V;
CC IsoId=p57727-4; Sequence=VSP_005394;
CC TISSUE SPECIFICITY: Expressed in many tissues including fetal
CC cochlea. Isoform T is found at increased levels in some
CC carcinomas.
CC -1- PTM: Undergoes autolytic activation.
CC -1- DISEASE: Defects in TMPRSS3 are a cause of childhood-onset
CC autosomal recessive neurosensory deafness 8 (DFNB8) [MIM:601072].
CC -1- DISEASE: Defects in TMPRSS3 are a cause of congenital autosomal
CC recessive neurosensory deafness 10 (DFNB10) [MIM:605116].
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 1 SRCR domain.
CC -1- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

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OM protein - protein search, using sw model

Run on: January 6, 2004, 09:58:56 ; Search time 40 Seconds
(without alignments)
3683,701 Million cell updates/sec

Title: US-09-978-194A-132
Perfect score: 3108
Sequence: 1 MLSSLSVLAGSVIAMI...PEPAEPCSLANISQPTSC 571

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP:invertebrate:*
6: SP:mammal:*
7: SP:mhc:*
8: SP:organelle:*
9: SP:phage:*
10: SP:plant:*
11: SP:rodent:*
12: SP:virus:*
13: SP:vertebrate:*
14: SP:unclassified:*
15: SP:rvirus:*
16: SP:bacteriap:*
17: SP:archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1868.5	60.1	426	11	08CFX9
2	724	23.3	766	4	08BNY4
3	481.5	15.5	328	11	08BUB6
4	451.5	14.5	799	11	09DBI0
5	448	14.4	327	4	08N171
6	447	14.4	284	4	08NFB6
7	438.5	14.1	1524	13	091674
8	436	14.0	331	11	08B1A6
9	425	13.7	802	4	081UE2
10	425	13.7	811	4	081UE0
11	418	13.4	339	11	0891A4
12	412	13.3	340	11	08B0V6
13	405	13.0	317	13	09GCR3
14	397.5	12.8	297	11	08B781
15	394.5	12.7	974	13	090WD8
16	384.5	12.4	1004	13	P79953

17	380	12.2	321	4	096RZ8	096RZ8 homo sapien
18	378	12.2	389	13	09PVX7	09PVX7 xenopus lae
19	375.5	12.1	812	11	09R0M3	09R0M3 ratius norv
20	371.5	12.0	812	11	091W05	091W05 mus musculu
21	369.5	11.9	329	13	042272	042272 xenopus lae
22	368.5	11.9	855	11	09J017	09J017 ratius norv
23	364.5	11.7	334	6	046507	046507 papio hamad
24	364	11.7	423	11	08BM10	08BM10 mus musculu
25	361.5	11.6	422	4	08WVC1	08WVC1 homo sapien
26	360.5	11.6	810	4	015146	015146 homo sapien
27	356.5	11.5	371	11	08CJ16	08CJ16 ratius norv
28	356.5	11.5	445	11	08CJ17	08CJ17 ratius norv
29	351	11.3	454	6	046506	046506 papio hamad
30	349.5	11.2	453	11	08VDE0	08VDE0 mus musculu
31	349	11.2	624	11	09DAT3	09DAT3 mus musculu
32	348.5	11.2	453	11	08K1T0	08K1T0 mus musculu
33	347.5	11.2	455	11	08CDR0	08CDR0 mus musculu
34	345	11.1	581	4	09BYE2	09BYE2 homo sapien
35	344	11.1	667	5	09B0M1	09B0M1 trichinella
36	343	11.0	335	11	08VIF2	08VIF2 mus musculu
37	343	11.0	624	11	091Y47	091Y47 mus musculu
38	343	11.0	806	6	018783	018783 macropus eu
39	342.5	11.0	282	11	09D4I3	09D4I3 mus musculu
40	342.5	11.0	322	11	0920S2	0920S2 mus musculu
41	342.5	11.0	537	4	09BYE1	09BYE1 homo sapien
42	340.5	11.0	624	6	095ME7	095ME7 oryctolagus
43	339	10.9	310	11	091XC4	091XC4 mus musculu
44	337.5	10.9	471	11	08CFE0	08CFE0 mus musculu
45	336.5	10.8	490	11	0920K3	0920K3 ratius norv

ALIGNMENTS

RESULT 1

08CFX9 PRELIMINARY; PRT; 426 AA.
AC 08CFX9;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Similar to protease, serine, 8 (Proctasin) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC039632; AAH39632.1; --
KW Protease.
FT NON_TER
SQ SEQUENCE 426 AA; 45483 MW; 7070BC4E20FAA862 CRC64;

Query Match 60.1%; Score 1868.5; DB 11; Length 426;
Best Local Similarity 80.0%; Pred. No. 2.3e-131;
Matches 339; Conservative 21; Mismatches 63; Indels 1; Gaps 1;

QY	148	ALLQLAHPTTHTPLCPQPAHFRPGASCWATGMDQDTSADAPGTLRNLRILISPTCNC	207
DB	4	ALLQTHPTVQTTLLCPQTYHFPFGACWATGMDQNTSDVSRTRLRNLRILISPTCNC	63
QY	208	INQCHQRLHSNPAPRPMICGSPQGVQPCQDGGGPRVLCLEPDGHVYQAGIISFASGC	267
DB	64	LVNRHQRLHSNPAPRPMICGGAQGEQPCQDGGGPRVLCLEPDGHVYQAGIISFASGC	123
QY	266	AQEDPVLITTPAAISSWLOARVQGAFLAOSPPETPMESDESDSCVACGSLRTAGPQAGAP	327
DB	124	AEQEDPVLITTPAAISSWLOAHVHEALFLVQAPGVKVSDESDSCVACGSLRTAGPQAGAL	183
QY	328	SPWPPEARLMHOGULACGALVSEBAVLTAHCFIGROAPBEMSVGLGTRPEWGLKOLI	387

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Db 184 SQMPPDARLKHGKMLCGGALVSEVVLTAHCFIRQTLLEBSVGLGAPBEEMGLKQI 243
Qy 388 LHGAYTHPEGGYDMALLLLAOPVTLGASLRPLCLPYDHLDPDGENWVLGARPAAGIS 447
Db 244 LHGAYTHPEGGYDVAFLLLAQPVTLGPRGLPLCLPADHLLPDGHWLGLGLQK-AGIN 302
Qy 448 SIQTVPVTLGPRACGRLLAARPGDSSPLPGMVCISANGELSPCGSLGAPLVHEVGT 507
Db 303 YPQYVAVTLGPMACGRHAAAPGCTGIPILPGMVCITTVGPEPHCGSLGAPLVHEIRST 362
Qy 508 WFLAGLHSEFGDACQGPAPPAVFTALPAYEDWVSSLDWQYFAPEEPPEAPSPCLANISO 567
Db 363 WFLVGHSGDTCQSSAKPAVFAALSAIEDWISLNDWQYFAPEEPPEAPSPCLANISO 422
Qy 568 PTSC 571
Db 423 PASC 426

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RESULT 2

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Q8BNBY4 PRELIMINARY; PRT; 766 AA.
ID Q8BNBY4
AC Q8BNBY4;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DE Hypothetical protein FLJ90661.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto Y., Wakamatsu A., Nakamura Y., Kojima S., Nagahata K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AK075142; BAC11431.1; -
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser protease.
DR Pfam; PF00089; trypsin; 3.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 3.
DR PROSITE; PS50240; TRYPSIN_DOM; 3.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hypothetical protein; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 766 AA; 82564 MW; 3630D550C806BD5 CRC64;

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Query Match 23.3%; Score 724; DB 4; Length 766;

Best Local Similarity 35.4%; Pred. No. 11e-45;

Matches 179; Conservative 68; Mismatches 189; Indels 70; Gaps 18;

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Qy 108 WSVVLSLQREGSLGAEVEVVAALQLPRAVNYHSGSDLAALQIAHPTT-----HTPLCL 163
Db 12 WSVLVGHSHQSDPLDGAHTRAVAAIVPANYSQVELGADALRLASPGAPAVPVCL 71
Qy 164 POPAHRFPFGASCWATGW-----DQDTSAPGTLRLRLRLISRPNCNCYINQLOHRLSN 219
Db 72 PRASHRFPVAGTACWATGMDVQADPLPLPVWLQGEVLRLLGEALTCQCLISQPGFNLTL 131
Qy 220 PARPMLCGGPPGPGVQGGSGGPRVLCLEPDGHVWVAGIISFASSCAQEDAPVLLINT 279
Db 132 QILPMLCAGYEGGRDTCQDSDGGLVYC-EEGGRWFQAGISFSGGRNRPRGVFTAV 190
Qy 280 AAHSSMLQARVGA-----AFLAQSPET-----ACGSLRTGPPAGAPAS 328
Db 191 ATTEAMIREQVWGSSEPPAFPTQPKTQSDPQEPRENCITLAPCG-----KAPRPG 243

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Qy 329 PWPWEARLMHQQLACGALVSEAVLTAHCFIRQAPPE-----WSVGLGTRPBEW 381
Db 244 AMPWEAQVWVPGSRPCHGALVSESVVLAPASCFLDPNNSDSDPPRLDAMRVLLPSPRAE 303
Qy 382 GLKQILMGATHPREGGYDMALLLLAOPVTLGASLRPLCLPRPDHLLDGER-----GNVL 437
Db 304 RVARLVQEHNSW--DNASDLALLQRTPVNLAAARPVCLPPEHYFLPGSRCLARW-- 360
Qy 438 GRARGAIISSIQVTVLLGPRACSRLLAAAPG-----DGSPLIPGVCIS--AVGELPS 491
Db 361 GRGEFALPGAL--LEALLGGMWCHCLYRGGAAPVPLPGDP--PHALCPAYQKEEYGS 416
Qy 492 CEGISGAPLVHEVRGTWFLAGLHSEFGDACQGPAPPAVFTALPAYEDWVSSLDWQYF-- 548
Db 417 CWNDSRWGLLCQEGEGTWFLAGIRDPSGC---LRPRAPFPQLQTHGFWISHTRGAVLYDQ 473
Qy 549 -----AEPPE-----PEAPRSGC 561
Db 474 LAMDGPDGEETETQTCPPHTEHGAC 499

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RESULT 3

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Q8BJR6 PRELIMINARY; PRT; 328 AA.
ID Q8BJR6
AC Q8BJR6;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE The FANTOM Consortium.
DE Similar to MARPSIN precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK080281; BAC37864.1; -
SQ SEQUENCE 328 AA; 35789 MW; DCOB20F1AB3EB840 CRC64;

```

Query Match 15.5%; Score 481.5; DB 11; Length 328;

Best Local Similarity 36.1%; Pred. No. 5e-28;

Matches 99; Conservative 46; Mismatches 112; Indels 17; Gaps 6;

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Qy 60 NTVPGEMPMQASVPROGAHICGSLVADTWLTAHCFEKAATELNSWSVLSLOREG 119
Db 43 NALGEMPMQVSIQRNGIHFGGSLIAFTWLTAAHCFSN--TSDISIVYLGLALKQ 100
Qy 120 LSPGAEVGAALQLPRAVNYHSGSDLAALQIAHPTT-----PLCLPPAHRFPFGAS 175
Db 101 PGPAHLYPVQVQVSNPDYQGMASADVALVELQGPVFTNYILPVCLPDSVSIFESGMN 160
Qy 176 CWAIGW-----DQDTSAPGTLRLRLRLISRPNCNCYINQ-LHPRHLSNPARPGMLCGP 230
Db 161 CWVVGMSQSPSODRLPNPRVLOKLAVPILIDTPKCNLLYNNKVESDFOLKTKIDMLCAGF 220
Qy 231 QPGVQPGCGSGGPRVLCLEPDGHVWVAGIISFASSCAQEDAPVLLINTAAHSSMLQARV 290
Db 221 AEGKDKACKDSSGSPVLCI-VDQSWVQAGVSWEGGCARRNRPRGVYIRVTSHKHIIQIT 279
Qy 291 QGAFFLAQSPETPEMSDESDSCVACGSLRTAGPQA 324
Db 280 PELQFQGRAGTQQQKXDSQ-----GQQRILGNSA 308

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RESULT 4

Q9DB10

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619 TVEFLGMRQNSWMPGEVSEFKVSRLFLPHYHEBDSHDYVALQLQDHPVVSATVRPVCPLP
QY 165 QPAHRPPFPASCSWATGMDQDSDAD--GTLRNLRLRLISPTNCICTYNOJLHRLNSPAR 222
Db 679 ARSHFEPEPQCHWIMTGMWAQOREGGEVSNLTQCKVDVQVLDPDCLSEAVRY-----QVS 730
QY 223 PGMLCGGPPOGPGVQGCOCGDSGSPVLCLEPDDCHWVQAGIISPASSCAQEDAPVLLTNTAAH 282
Db 731 PFMLCGIRKKKAKDCQGDSSGSPVLCREPSGRMLAGLVKGLCGAPNFFGYTRVTRY 790
QY 283 SSWLQ 287
Db 791 INWIQ 795

RESULT 5
Q8NI171 PRELIMINARY: PRT: 327 AA.
AC Q8NI171:
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Similar to proctase, serine, 8 (Proctasin) (Fragment) .
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Straussberg R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; BC036846; AAH36846.1; .
DR Interpro: IPR001314; Chymotrypsin.
DR Interpro: IPR001254; Ser. protease_Try.
DR Pfam: PF00069; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRPSIN.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Hydrolyase; Protease; Serine protease.
FT NON_TER
SQ SEQUENCE 327 AA; 35106 MW; 60458ED817AC1CF3 CRC64;

Query Match 14.4%; Score 448; DB 4; Length 327;
Best Local Similarity 41.0%; Pred. No. 1.6e-25;
Matches 100; Conservative 32; Mismatches 84; Indels 28; Gaps 7

QY 64 GEMPWQASVYRQGAHICSGSLVADTWVLTAAHCEKAAATELNSWSVLSLQREGSLSPG 1233
Db 93 GEMPWQASVYRQGAHICSGSLVADTWVLTAAHCEKAAATELNSWSVLSLQREGSLSPG 150
QY 124 AEEVGYALQLPRAYNNHKSQGSDLALLQLAHPHTHT---PLCLPQPAHRRPPGASCMAT 179
Db 151 TLTSPVRRVLLPPDYSESGARGLDALQLARRPVPLSARVQVCLPVGARPPTGRCVTV 210
QY 180 GMDQDSDAPGTF-----LNLRLRLRLSRPTNCIYV-----QLHRLHNSNARPGML 226
Db 211 GMS---SLRPGVPLPEMRPLQGVRRVPLDLSRTCGLYHVGADVQARIVL----PGSL 262
QY 227 CGPQPGVQVGPQCGSDSGPFLCLEPDDGHVQAGIISPASSCAQEDAPVLLTNTAAHSSWL 286
Db 263 CAVYRPGHMDACQGDSSGSPVLCLEPDDGHVQAGIISPASSCAQEDAPVLLTNTAAHSSWL 321
QY 287 QARV 290
Db 322 QARV 325

RESULT 6
Q8NFB6

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ID 08NF86 PRELIMINARY; PRT; 284 AA.
 AC 08NF86;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Serine protease EOS.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Darrow A.L., Qi J., Andrade-Gordon P., Chen C.;
 RT "DNA encoding the human serine protease EOS.";
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL: AF536382; AAN0405.1; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR PRINTS: PR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin; 1.
 DR SMART: SM00020; tryp; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydroxylase; Protease; Serine protease.
 SK SEQUENCE 284 AA; 30110 MW; FDF3F1750D569978 CRC64;

Query Match 14.4%; Score 447; DB 4; Length 284;
 Best Local Similarity 40.7%; Pred. No.1.6e-25;
 Matches 101; Conservative 31; Mismatches 88; Indels 28; Gaps 7;

QY 64 GEMPMQASVRRQAGHICSGSLVADTWLTAAHCFEKAATELNSWSVLGSLQREGISPG 123
 DB 46 GEMPMQASIGHPAHVCGSLINPQWLTAAHCFPRALPA--EYVRLGALRLGSTR 103
 QY 124 AEEVGVAAALDPRAYNHYSQSDLLALLQLAHPHTHT---PLCLPQPARHFRPGASCWAT 179
 DB 104 TLEVPARRVLLPRDYSEDGARGLALLQLRRPVLRSARVQPVCLPYPGARPPGTPCRVY 163
 QY 180 GMDQDSDAPGT-----LRNLRLRLISPTGNCIYN-----OLHQRHLSNPARPGM 226
 DB 164 GWC---SLRPGVLLPEWRPLQGVRLPDLSDRTCDGLHVGADVPQERIVL-----PGSL 215
 QY 227 CGGPGQGVGVRCCGSDGSPVLCLEPDGHWVQAGIISFASCAQEDAPVLLTNTAAHSSWT 286
 DB 216 CAGVPGHKAQCGDGGGRLTCLD--SGSWLVGVVWGKGCALPNRPVYTSVATISPMI 274
 QY 287 QARVQGA 294
 DB 275 QARVTSNA 282

RESULT 7

ID 091674 PRELIMINARY; PRT; 1524 AA.
 AC 091674;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Polypeptin.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99432219; PubMed=10500163;
 RA Lindsay L.L., Yang J.C., Hedrick J.L.;
 RT "Ovocytinase, a Xenopus laevis egg extracellular protease, is
 translated as part of an unusual polypeptide.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:11253-11258(1999).

RN [2]
 RP SEQUENCE FROM N.A.
 RA Yang J.C., Lindsay L.L., Hedrick J.L.;
 RT "CDNA Cloning of Ovocyasinase, a Chymotrypsin-like Protease Released
 From Xenopus laevis Eggs at Fertilization.";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 4 CUB DOMAINS.
 DR EMBL: U01290; AAC24717.1; -;
 DR HSSP: P00763; IDPO.
 DR MEROPS: S01.022; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000859; CUB domain.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00431; CUB; 5.
 DR Pfam: PF00089; trypsin; 3.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00042; CUB; 4.
 DR SMART: SM00020; tryp; 3.
 DR PROSITE: PS01180; CUB; 5.
 DR PROSITE: PS00240; TRYPSIN_DOM; 3.
 DR PROSITE: PS00134; TRYPSIN_HIS; 3.
 DR PROSITE: PS00135; TRYPSIN_SER; 3.
 DR Hydroxylase; Protease; Serine protease.
 FT CHAIN 57 308
 FT CHAIN 584 817
 FT CHAIN 1295 1524
 SK SEQUENCE 1524 AA; 167566 MW; 32EFB42128F37268 CRC64;

Query Match 14.1%; Score 438.5; DB 13; Length 1524;
 Best Local Similarity 18.8%; Pred. No.4.9e-24;
 Matches 147; Conservative 97; Mismatches 211; Indels 327; Gaps 20;

QY 59 GNTVGEPMQASVRRQAGHICSGSLVADTWLTAAHCFEKAATELNSWSVLGSLQREGISPG 118
 DB 61 GDAVVGQGVWTSLSLNERHICGSIYKRDVNTAAHCVYPTETELKVSMTYIVGEYDQ 120
 QY 119 GLSPGAEEVGVAAALD-LPRAVNHYSQSDLLALLQLAHP---TTHPTCLPQPARHFRPG 173
 DB 121 VMDSQEQSLPVSHIEHPHRYRGDGMGYDALVFLSKPLIFSGVQPICLPVGKEIEAG 180
 QY 174 ASCWATGMD--ODTDAPGTLENLRLRLISPTGNCIYNOLHQRHLSNPARPGMISCGPQ 231
 DB 181 TCVSSGWRLEENDLSVLQEVKLPVVDNCTCAVLEIGHVPLDDT---MCAGRP 236
 QY 232 PGVQPGCGSDGSPVLCLEPDGHWVQAGIISFASCAQEDAPVLLTNTAAHSSWT 278
 DB 237 EGMDACQDSDGSPVLCRRRSGVWFLAGCVSGLGCGRSWAKQIIRSGSGPAIFSRVS 296
 QY 279 -----TAHSS-----WLOA----- 288
 DB 297 SVLDPLRPKLLGGCGSSKRTITGKNGTVRYPLSGNYSINSYCRMWLAQKATIEIRFL 356
 QY 289 ----- 288
 DB 357 QLDIEDHATCFDYLSFTVNEKIRKVCSTIPSLIVRSNKVTVTFPSDGTFTGRGEI 416
 QY 289 -----RVQGAALASPEI----- 302
 DB 417 QFLAIPTKAASGSAKILKKGMIVSPNYPDPYPLKCTSWITEAPENHIVLKFEEDN 476
 QY 303 -----PEMSDEDSCV----- 312
 DB 477 VEGHGCTDAVEVVDGAEEKOLIALRCGYTLPPLISSPENTMLIRFKTDMENSYGRFV 536
 QY 313 -----ACGSL-----RTAGPQAGAPSPWP 331
 DB 537 KFSFVPEKEQFSLPYDDTPTISMLHPRATLDVCGMAPWTPKMWLPRIYVGEASPSNWP 596
 QY 332 WEARLHQQLACGALVVEEAVLTAHCFITGRQAPBEESVGLG-----TREBEMWL 383
 DB 597 WVOVIFLRTFCEGALISPMWILTAHCFITGRQAPBEESVGLG-----TREBEMWL 655

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QY 384 KQILLHGAYTHPEGGYDMLALLLAQPTVLGASLRPLCLPYDPHHLPGDE----RGM--VL 437
DB 656 KTIHIDHYNSETYDNDIALLIYLEBPLDLDNFVRVCLPEPEEVLTPASVCVWTGWNNTA 715
QY 438 GRAPPGAGISSIQTVPVTLTGPRACSRLLHAPGCGSGPILPGMVTSAV--GEL----- 489
DB 716 EDGQPALGLOQLD-----PILDSITICNTSYSGELTDHMLC 752
QY 490 ---PS-----CEGISGAPLVHEVNGTWF-LAGLHSPGDACQGPAPRAVFTALPAYEDWV 539
DB 753 AGPSSSKEXDACQGDSSGGLVCQNEKEQFSIYGLVSWEGGGRVSKPGVTKVRLFFFTWI 812
QY 540 SS 541
DB 813 QN 814

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RESULT 8

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Q8RIAG PRELIMINARY; PRT; 331 AA.
AC Q8RIAG;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE RIKEN CDNA 2010001P08 gene.
GN 2010001P08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RE SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024903; AAH24903.1; -.
DR HSSP; P00761; IANI.
DR MGD; MGI:1917064; 2010001P08RIK.
DR Interpib; IPR001254; Ser.protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSTIN_DOM; 1.
DR PROSITE; PS00134; TRYPSTIN_HIS; 1.
DR PROSITE; PS00135; TRYPSTIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 331 AA; 35639 MW; C06F6EF2FA261636 CRC64;

```

Query Match 14.0%; Score 436; DB 11; Length 331;

Best Local Similarity 35.9%; Pred. No. 1.2e-24;

Matches 98; Conservative 47; Mismatches 102; Indels 26; Gaps 9;

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QY 53 GKAKHGNTVGE-----WPMQASVRROGAHICGSGSLVADTWVLTAAHCFEKAATLNLN 106
DB 46 GRPRSGIVSGQDAQLGRWPQVSVRENGAIVCGGSLAEWVLTAAHCFEGGOS--LS 103
QY 107 SMSVVLGSLQREGSLPGAEVGVAA--LQLPR-AVNHYSQGSDDLALQLAHTTHT---- 159
DB 104 IYTVLGLTSSYPEDNEPKELRAVAQFIKHPSYADHSSG--DIALVQLASPIINDMYL 162
QY 160 PLCLFQPAHRPPFGASCATGMDQDTSD---APGTLLNRILRLISPTCNCIYNQLHOR 215
DB 163 PVCLPFPKPDPLDPGTMCWTGWHIGTQPLRPPTLQELQVPLIDAETCMTYQENSIP 222
QY 216 HLSNARPGMLCGSGPGVCGSGDGGGPGVLCLEPDDGHVWAGLISFASCAQEDAVYL 275
DB 223 GTEPVILGMLAGHQGGKKAQCNDSGGPLVC-DINDVWIDAGVAVSWGSDCALFKRPQV 281
QY 276 LTNTAAHSSMLQ-----ARVGAALFAGSPETP 303
DB 282 VTNVSVYISWINTMTMNLPMERGRGSPSLSGTP 314

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RESULT 9

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Q8IU82 PRELIMINARY; PRT; 802 AA.
AC Q8IU82;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Matrilpase-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RE SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=22241917; PubMed=12149247;
RA Velasco G., Cal S., Quesada V., Sanchez L.M., Lopez-Otin C.;
RT "Matrilpase-2, a membrane-bound mosaic serine proteinase predominantly
RT expressed in human liver and showing degrading activity against
RT extracellular matrix proteins.";
RL J. Biol. Chem. 277:37637-37646(2002).
DR EMBL; AJ319876; CAC05953.1; -.
SQ SEQUENCE 802 AA; 88901 MW; C30D37BEC4F1D22E CRC64;

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Query Match 13.7%; Score 425; DB 4; Length 802;

Best Local Similarity 35.4%; Pred. No. 2.3e-23;

Matches 87; Conservative 39; Mismatches 106; Indels 14; Gaps 3;

```

QY 48 VOEPQGAKKRNGTVPPEWPMQASVRROGAHICGSGSLVADTWVLTAAHCFEKAATELNS 107
DB 561 LQGPSSRIVGAVSSBGEWPMQASLQVRGRHICGALILADRWVLTAAHCFQEDSMATVYL 620
QY 108 WSVVLGSLQREGSLPGAEVGVAA--LQPRAYNHYSQGSDDLALQLAHTTHT----PLCL 163
DB 621 WTVFLGKRWQNSRMNGEVSFVVSRLLLHPYHEEDSHYDVALQLDHPVRSAAVPRVCL 680
QY 164 PQPAHRPPFGASCATGMDQDTSAP--GTLRLRLRLISPTCNCIYNQLHQRHLSNPA 221
DB 681 PARSHFEPFGIHCWITGVALREGGPISNALQKVDVLLIPDLCSEVRY-----QV 732
QY 222 RPKMLCGSPGPGVCGPGDGGGPGVLCLEPDDGHVWAGLISFASCAQEDAPVLTNTAA 281
DB 733 TPRMLCAGYRKQKDKDQCGSGPLVCALSGRFLGLVSWGLGCGRPNGVYTRITG 792
QY 282 HSSWLQ 287
DB 793 VISWID 798

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RESULT 10

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Q8IU80 PRELIMINARY; PRT; 811 AA.
AC Q8IU80;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Type II transmembrane serine protease 6.
GN TMPSR56.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RE SEQUENCE FROM N.A.
RA Hooper J.D., Quigley J.P.;
RT "TMPSR56, a new type II transmembrane serine protease.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055383; AAL16413.1; -.
DR EMBL; AY055384; AAL16414.1; -.
KW Protease; Transmembrane.
SQ SEQUENCE 811 AA; 89999 MW; 7EEF193F655DDEBD CRC64;

```

Query Match 13.7%; Score 425; DB 4; Length 811;

[illegible]

Best local similarity 35.6%; Pred. No.2,98-23;
Matches 99; Conservative 41; Mismatches 101; Indels 26; Gaps 6

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QY 59 GNTVPGWEPWQASVYRROGAHICSSGLVADTVYVLTAAHCFEAAATELMSWSVLSGLORE 118
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 49 GSAKPGCWPMQOVSIITYDGNHVCGSLVSNKVVSAACHFEHRE--AYEVKGAHQLD 106
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 GLSPGAEVVAALQLPRAVNHYSQSGDALLLOLAHPHTTH----PLCLPQARHPFGA 174
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 107 SYSDYIVVHTVAQIITHSSVREBSQGDIALIRLSSPTTSRYRPICLPAAHNSFPMGL 166
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 SCWATGW----DQDTPDAPGLTRNLRLRLISRPNCIYNQLHORHLSNPARPGMLCGSP 230
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 167 HCYVTGNGHVAAPSYSIQTPRPLQLLEVPILSRCTSCGLYNINAVBEPHTIQDDLCAGY 226
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 231 QPVGVCQCGDSSGSPVLCLEPDGHVWVAGIISFSSCQAEQAPVLLINTAAHSSV----- 285
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 227 VKGSKDACCQDSSGFLSC-PMEGIVYLAGIVSWGDACGAPRPGVYTLTTSYASWIRHHV 285
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 286 --LQARVQGAAPLAQSPETPE 304
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 286 AELQPRV-----VQTOR 298
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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ID	Q99L44	PRELIMINARY;	PRT;	339 AA.
AC	Q99L44;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Similar to protease, serine, 8 (Proteasain).			
GN	PRSS8.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
ON	[1]_TaxId=10090;			
RP	SEQUENCE FROM N.A.			
RA	Strasberg R.;			
RL	Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/SvJ, and Swiss; TISSUE=Lung;			
RA	Vergnes G.M., Caughey G.H.;			
RT	"Molecular Cloning and Characterization of mouse prostasin, a type I			
RT	membrane-associated serine protease of the gamma-tryptase/prostasin			
RT	gene family.";			
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Kitamura K., Takefumi N., Kimio T.;			
RT	"mouse serine protease.";			
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
DR	EMBL, BC003851, AA03851.1; -			
DR	EMBL, AF378086, AAL06320.1; -			
DR	EMBL, AF378085, AAL06319.1; -			
DR	EMBL, AB038244, BAB82496.1; -			
DR	HSSP: P00734; IUVS.			
DR	MGI: 1923810; Prss8.			
DR	InterPro: IPR001314; Chymotrypsin.			
DR	InterPro: IPR001254; Ser_protease_Try.			
DR	Plan: PFO0089; trypsin; 1.			
DR	PRINTS: PR00722; CHYMOTRYPSIN.			
DR	SMART: SM00020; TRY-SPC; 1.			
DR	PROSITE: PS00240; TRYPSIN_DOM; 1.			
DR	PROSITE: PS00134; TRYPSIN_HIS; 1.			
DR	PROSITE: PS00135; TRYPSIN_SER; 1.			
KW	Hydrolase; Protease; Serine protease.			
SEQUENCE	339 AA; 36216 MW; BC02688BC057AF10 CRC64;			

ID	Q8BJV6	PRELIMINARY;	PRF;	340 AA.
AC	Q8BJV6;			
DT	01-MAR-2003 (TREMBlrel. 23, Created)			
DT	01-MAR-2003 (TREMBlrel. 23, Last sequence update)			
DT	01-MAR-2003 (TREMBlrel. 23, Last annotation update)			
DE	Proctasin.			
OS	Mus musculus (Mouse).			
OC	Eukaryote; Metazoa; Chordata; Cranista; Vertebrate; Euteleostomi;			
OC	Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Eye;			
RX	MEDLINE=22354685; Pubmed=12466851;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RL	60,770 full-length cDNAs."			
DR	Nature 420:563-573(2002).			
DR	EMBL; AK078696; BAC37362.1; '-.			
SQ	SEQUENCE 340 AA; 36503 MW; 3C2540E9B3A81C8A CRC64;			
QY	Query Match	13.3%;	Score 412;	DB 11; Length 340;
QY	Best Local Similarity	35.8%;	Pred. No. 7.9e-23;	
QY	Matches 92;	Conservative 39;	Mismatches 100;	Indels 26; Gaps 6
QY	63	PGEMPMQASVVRQGANHICGSLVADTVTLTAANCFFEAATELNSWSVVLQREGISL	122	
QY	54	FGGMPQWVSTLYGDNHVCGSGIVSNKKVVSAAHCFPREHSE--AYEVKLGDHQDLDSYN	111	
QY	123	GAEVGYAALQLPRAYNHVYQGSDDLALLDLAHPPTH---PLCLROPANRFPFGASCWA	178	
QY	112	DTVHTVAQIITHTSSYREEGSQGDIALIRLSSPYTFERYIRPICLPANASFPNGLHCTV	171	
QY	179	TGW----DQPTSDAPGTLRLRLRLISRPNCNCYUNLQHNHNSNPARGMLCGSPQGV	234	
QY	172	TGGWHAHSVSLQTPRLQCLEVPLISRETSCLYNNANVDEEPTTIQDMLCAGYVKG	231	
QY	235	QGFQGGSGGSPVLCLEPDGHVWVGAGISFASSCAQEDAPVLLTWTAAHSSW-----LQ	287	
QY	232	KDAGCGSGSGPPLSC-PMEGIIWYLAGIVSKGDACAPRPGVYTLITSTYASHIHHVABLQ	290	
QY	288	ARVQGAFLAQSPTPE 304		
QY	291	PRV-----VPQTQE 299		

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RESULT 13
Q9DGR3 PRELIMINARY; PRT; 317 AA.
AC Q9DGR3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Emryonic serine protease-1.
GN XESP-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20363741; PubMed=10903452;
RA Yamada K., Takabatake T., Takeshima K.;
RT "Isolation and characterization of three novel serine protease genes
from Xenopus laevis."
RL EMBL, AB038496; BAB08216.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.048; -.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 317 AA; 34413 MW; EEC78A9F46D138FE CRC64;

Query Match 13.0%; Score 405; DB 13; Length 317;
Best Local Similarity 33.2%; Pred. No. 2.4e-22;
Matches 89; Conservative 45; Mismatches 106; Indels 28; Gaps 7;

QY 60 NTVPGEWQASVRRQAHICGSLVADTWVLTAAHCEKAAATELNSWVVLGSLQREG 119
DB 48 DTRQAMPQVSLFENGSHICGSIISDQWILTATGCIHPDLF--SGGVNLGAYQYLV 103
QY 120 LSPGAEVGVNALLQPRVANHYSQGSDDLALLQLAHPHTHT---PLCLPQPAHRRPFQAS 175
DB 104 KNPHEMTVAVVDIIYINSEFNGPGTSGDIALKLSSPIKFTXYILPICFPASVPTSSGSE 163
QY 176 CWATGMDODTSDA---PGLRLRLRLISPTCNCIYQLQRHLSNP-----ARPG 224
DB 164 CHTTGNGGTGSEVPLQYPTLQKVMPTINRDSCEKMT-----HNSVISTETILLQSD 217
QY 225 MLCGGPQPGVQPCQCGDSGGPVLCLEPDGHWVQAGIISPASSCAQEDAPVLLTNTAAHSS 284
DB 218 QICAGVQAGQKXQCGDSGGPLVC-KIQGFVQAGIVSGERCACKNRGVVTFVPAYET 276
QY 285 WLQARVQGAFLAQSFEPTPEMSDEDSVCV 312
DB 277 WISER----SVISFKPTSSSSPSSSV 300

RESULT 14
088781 PRELIMINARY; PRT; 297 AA.
AC 088781;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Serine protease precursor (Fragment).
GN BSP2.
OS Rattus rattus (Black rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10117;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=Fisher; TISSUE=Brain;
RX MEDLINE=96389725; PubMed=9722524;
RA Davies B.J., Pickard B.S., Steel M., Morris R.G., Latche R.;
RT "Serine Proteases in Rodent Hippocampus."
RL J. Biol. Chem. 273:23004-23011(1998).
DR EMBL; AJ005642; CAA06644.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.252; -.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolyase; Protease; Serine protease; Signal.
FT SIGNAL 1 23
FT NON TER 1 1
FT SIGNAL <1 23
FT CHAIN 24 297 SERINE PROTEASE.
SQ SEQUENCE 297 AA; 32086 MW; 6DA25C6633D6AB55 CRC64;

Query Match 12.8%; Score 397.5; DB 11; Length 297;
Best Local Similarity 34.2%; Pred. No. 8.2e-22;
Matches 92; Conservative 47; Mismatches 105; Indels 25; Gaps 9;

QY 53 GKAKRHGNTVPGF-----WQASVRRQAHICGSLVADTWVLTAAHCEKAAATELN 106
DB 32 GKPOLNRVVGGEPSADQWPFIVSIILKNGSHHCAGSLITRWVWVSAHCF--SSMDKPS 90
QY 107 SMSVVLGSLQREGSPGAEVGVNA-LQPRVANHYSQGSDDLALLQLAHPHTHT---PL 161
DB 91 PYSVLLGAMKLGNDPSPQKVGIVASVLPHPYRSKEGTHADIALVLERPIQFSERILPI 150
QY 162 CLPQPAHRRPFQASCWATGW----DQDTPDAPGTLRLRLISPTCNCIYNLQHRHL 217
DB 151 CLPSSVHLPEPNTMCWLAGWGSIDGVLPRLPQTLQKLVIIIDELCKSLY----WRGA 206
QY 218 SNPA-RPGMLCGPQPGVQPCQCGDSGGPVLCLEPDGHWVQAGIISPASSCAQEDAPVLL 276
DB 207 GQEAITEDMLCAGYLEGRDACLDSGGPLMC-QVDDHMLLTGIIISWEGCAERNRPGVY 265
QY 277 TNTAAHSSWLQARVQGAFLAQSFEPTPEMSDEDSVCV 302
DB 266 TSLLAHRRPVQRIVQGVQLRGLADSGDT 294

RESULT 15
Q90WD8 PRELIMINARY; PRT; 974 AA.
AC Q90WD8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Oviductin.
OS Bufo japonicus (Japanese toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Bufonidae; Bufo.
OX NCBI_TaxId=8387;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=oviductal pars recta;
RA Hi-yoshi M., Takamune K., Mita K., Kubo H., Sugimoto Y., Katagiri C.;
RT "Oviductin, the oviductal protease that mediates gamete interaction by
affecting the vitelline envelope in Bufo japonicus: Its molecular
cloning and analyses of expression and post-translational
activation."
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB070367; BAB63372.1; -.
DR HSSP; P00761; IANI.
DR MEROPS; S01.240; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000859; CUB_domain.

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DR InterPro: IPR001254; Ser_Protease_Try.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00089; trypsin; 2.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00042; CUB; 2.
DR SMART: SM00020; Tryp_Spc; 2.
DR PROSITE: PS01180; CUB; 2.
DR PROSITE: PS0240; TRYPSIN_DOM; 2.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KM Hydrolyase: Protease; Serine protease.
SQ SEQUENCE 974 AA; 107647 MW; F19705A470465553 CRC64;

Query Match 12.7%; Score 394.5; DB 13; Length 974;
Best Local Similarity 19.5%; Pred. No. 5.5e-21;
Matches 162; Conservative 83; Mismatches 213; Indels 373; Gaps 26;

QY 46 RKYQEPQGRKRRG-----NTVPEMPQASVRRQAHICSSGL 84
DB 20 RGVTDSPGRVSRGEPNANTSVSYGLISRIVGTSVAKGESPPMWVSLKRDGHFCGCTI 79
QY 85 VADTWVLTAAHC-----FEKAATELNSVVLGSLQREGSPGAEVGVNALQLP-- 135
DB 80 ISDKVLTAAHCYLEKNEFEQVSISGDHDFAYVERSEQRFAIK-----SVFKHPNF 131
QY 136 ---RAVNHYSQSDLLALLQLAHPTTH---TPCLPQPAHFPFGASCWATGMD--QDTS 186
DB 132 KPSRPENY---DLALTELVESITFDKDIQPACLSPDDVPFTGTLQMALGWRGLQENG 186
QY 187 DARGTLRNLELRLLISRTCNICYNQHLRLSNPARGMLCGPGQVQVCGCCGDSGGPV 246
DB 187 RLPSSTLQKVVLPLEIYRRCISIMETVDR---LAFETVCAQFPFGKDCQCGDSGGPF 242
QY 247 LCLEPDGHWVQAGIISFSSCAQ-----EDA 272
DB 243 LCGRSQGRWLVGVTSWGLCGARKMADNILDVESKSPGVFTDIQRLNWLSENINQDK 302
QY 273 P-----VLLT----- 277
DB 303 PDPPYQVQCSTNDIGIEKTTGELLPTGYKYYNNNEKCIWTIIVPRGHILLTFKSPN 362
QY 278 ----- 277
DB 363 VECDSYCDLDLVLYSALGRLIGKFCGDVSPRLLIADASTLKFISDFEYKTFGLFY 422
QY 278 -----NTAHSW----- 285
DB 423 EAVEPDTPSDCGSAVIFEEGEIQTMMHPLVSSHANCQVAVHSPANYITKITPLVE 482
QY 286 -----LQARVQGAAP----- 295
DB 483 VERSEGCIFDLVYVYHDLQGTVAAGFCFALPDVLSVSNVMQITFTSDYSANYLGPRA 542
QY 296 -----LAQSPETPE-----MSDEDC---VACGSLRTAGP-----OAGAP 327
DB 543 VISFVLPSSPVKPEKGNQNRKQNDAMQHPDECG---VSPLPFRFLYHNLIKAEAMP 598
QY 328 SPMPWEARLMHQQLACGALVSEEAFLTAHCFIGROA--PE-----EMSVGLG 375
DB 599 NSMPMHVSTINGKHYCNGAILSKTFVVSANCAVADREFFSIGLIVAGLHDLSSINTQ 658
QY 376 TREEMGLKQLIHGAYTHEEGYDMALLLAQPVTLGASLRPLCLPYPDHLLPDE--- 432
DB 659 KRREY---VIHPDYNRLSKDYDALIHVGRPPQYNSVYQPICLPDGHSLRLEPSKLCV 714
QY 433 -RGWVIGRAAPGAGISLQTVPTLLGPRACSRLLHAAPGGDSPIIPGMVCTSAVGE--L 489
DB 715 VSGMDNLVELS---TKLQLEVPVLMDDVCKKRY---DG--ITDRMFCAGVIAEDN 763
QY 490 PSCEGSGAPLV-HEVGTWFLAGLSFGDAGCGPARPAVFTALPAYEDMV 539
DB 764 ASCLAQSGAPLVQASAPGTIAFGIVSRGVGNETPRAGYSSVFLFIPWT 814

Search completed: January 6, 2004, 10:02:38
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